

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGACAGGACCTGGAGCTCCGGTGCCTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCCGCGCCGGGCCGCGCTGGGGCTCCTGCGCGCTTCGCTG
CTGCTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAAACAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGCGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCCGCTGTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGAGCAGACA
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGTGCAGAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCAGGAACTGTAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG
GAAGATGCCGTGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC
CGTGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTGCCCTTAAACAGCTGCATTTCTTGGTTGTCTCTTA
AACAGACTTGATATTTTGATACAGTTCCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCACTTGTATTATTCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTCAGTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTGCGGCAGCACCATGGCCTGAAAT
AACCTCTGAAGAGGAACCTTGTTAGGTACCTTCTGAGGCGGAAAGAACAGCTGTGGAATG
TGTGTCAATTAGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTTT

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FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKNFGGGNTAWEETLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYFDLFEWFCVKTLKVCSSPGTYGPDCLACQGGSRPCSG
NGHCSDGDSRGDSCRCMHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKCTCSGLTNRDCGCECVGWVLDE
GACVDVDECAAEPPPCSAQAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAETK
CVRKNENCYNTPGSYVCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

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FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCGCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTTGCG
GCACGAGGAGTTTTCGCCGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGGCCTGTACTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAACTTCTATGAATTCCTGTCTTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAACACAGGATGGGGTGGCAGCATTGAAAT
GGATGTGATTTGTTATGAATTCGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT
TCTTTAAAAACATGTCAACAGCTGAGTGCCAGGCCGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAAGCCCTTGT
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTAAATGGAGGGACC
TGTTTCTACCCTGGAATAATGATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCACAACCCCTGTGCAAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT
GGAACCTGCCATGAACCCAACAATGCCAATGTCAAGAAGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCCCAGCTCAGGCAGC
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTTCATAGCCTTTGTAAACCTTTCA
TGTTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGTCTGTAG
CATGATGTTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTAACATGCATTATGTT
GTCTGGGGGCAGGGGAACATCAGAAAGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGAGATTTTAGAT
GTTTGTTCATTTTAAAAAATGTCTTTAATTTTAAACTCTCAATACAATATATTTTGACC
TTACCATTATTCAGAGATTCAGTATTAACAAAAAATACTGTGGTAGTGGCATT
AAACAATATAATATTTCTAACACAATGAAATAGGGAATATAATGTATGAACCTTTTGTGAT
TGGCTTGAAGCAATATAATATATTGTAACAAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAAATAA
AAAAAATAAATAAATAAATAAAGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGCCCCAATTGTTTATTGCAGCTTATAATG

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FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGSKCKCSKGYQSDLCSKPVC
EPGCGAHGTCHPEPNKCQCQEGWHRHCNKRYEASLIHALRPAGALRQHTPSLKAEEERDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
 CCCCAGCCACACCTTACACAGGGGCCAGGAGCCACCATGTGGCGATGTTCACCTGGGGCTAC
 TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGTGGGCGCCGG
 GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
 GCAGGACCTGTGCTGCCGCGGCGGTGCGGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
 GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
 TGCCTCGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
 TCCAGTCTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT
 GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
 GAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCATTGCTACCGCCTGGGCACCA
 TCCGCCATCTTCTCCTCGGTGATGAACATGCATGAAATTATACAGTGTCTGAACCCAGGGGAG
 GTGCTTCCACAGCCTTTCGAGGCCCTCTGAGAAGTGGCCCAACCTGATTATGAGCCTCTTGA
 CCAAGGCAACTGTGCAGGCTCCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
 CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCAGAACCTGCTGTCTTGTGAC
 ACCCACCAGCAGAGGGCTGCGCGGTGGGCGTCTCGATGGTGCCCTGGTGGTTCTCGCTCG
 CCGAGGGGTGGTGTCTGACCCTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
 CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCC
 CACTGCCCCAACAGCTATGTTAATAAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
 CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
 TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
 CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
 AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
 CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCAGCGGCTCAATGAGTGGGACATCGAG
 AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTATCACTGAGGCTG
 CGGGCACCAACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
 GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
 CCCGGCGCGGTTCCGCTGACGCGAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
 GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
 ATCCCAGGCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
 CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
 TTGCCCAGGTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
 AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACACACACCTGGC
 TAATTTTTGTATTTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
 CTTGGGCTCAAGCGGTCCACCTGCTCCGCTCCCAAAGTCTGGGATTGCAGGCATGAGCC
 ACTGCACCCAGCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
 TAAACCAAAGTATTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPGLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTTCGTGTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCCTCATCAGCAAAGGCTG
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGGCAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGTGCAGCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCTGACCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTTCTCCACCCTTAACCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCGCACCCAGCA
GGGGACAGGCACCTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

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FIGURE 9

MTHRTTTWARTSRRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVCTPVPHDPFPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPASTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAG

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

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FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATCGGAGCCGCCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG
CGTGTTTACGGAGATCGTGCTGGAGAACTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTTATGGCCTTACGCGGCAGGGGGCGGCCCCGCCAGGCTTCCCCGAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCAACGC
CGAGAAGCAGAAGCAGTTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCGGGCGCCTCCC
CACCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTGAGCGACTGAAGGCCTTGCGAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTTGTGTTTGTGTTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCCTGC

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FIGURE 11

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLE
NNYTAFQONARHEGWFMATFTRQGRPRQASRSRQNRQEAHFQIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGAGATTATTTTAC
 CATACGCCCTCAGGAGCTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAAACCCCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTCTTTTCCCACCACATTGTATTTTAT
 TTCCGTACTTTCAGAAATGGGCCCTACAGACCACAAAGTGCCCCAGCCATGGGGCTTTTTTCTT
 GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCCTGCC
 CTAGTGTGTGCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGAGGGGCTAACCGTACTCTACCTCCACAACAACCAATTAATAATGTC
 TGGATTTCTGCAAGTGCACAATGTACAGTCCGTGTCACACCGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTACAGATTCTCCATTGTCAGGAAAAAC
 AATATTTCAGACCATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
 TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTTGGGCTTCCCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGTGTCTATATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGCGCTTATTTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACTTCAGCCATCTCAACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
 CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTCAGGACAACCAGAT
 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACTGAAGCAGCTC
 ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA
 ATATATCCCTTATCTCTCAACGTGCGGGGTTTTCATGTGCCAAGGCTCGAACAAGTCCGGG
 ATAGTGGCGGTGAGGGAATTAATAATGAATCTTTTGTCTGCTCCACCACGACCCCGGCTG
 CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
 TCCAAACCTTAGCAGAAGCTACACGCCCTCCAACCTCTACCACATCGAAACTTCCCAAGATT
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCGATCCACCTATCGGATT
 TGTTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGG
 CACCACCCTATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGTCATATGCCAAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAAATACAACCGGGGCGCGGGAAGATGATTTATTGCGAGGCAGGCACCAAGA
 AGGACAACCTCATCTCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCTCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTCAGACTGCAGCCCATTTACACCCCAATGGGGGCATTAAATTA
 CACGAGCTGCCATATCCCCAACAACATGCGATACTGCACAAGCAGCGTGCACAGCCTGGAGC
 ACTGCCATACGTCAGCAGCCAGAGCCAGCGTTATCAAGGCGGCAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTGGAATCTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTCTATTTCAAGTTAATTACAACAGTTTGTAACTCTTTGCTTTTAAATCTT

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FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLLEELHLDNDSISTVGVEDGAFREAI SLKLLFSLKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMVAVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWGGERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHEGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSVDPLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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FIGURE 14

ACTTGGAGCAAGCGGCGCGGCGGAGACAGAGGCGAGAGGCGAGAAGCTGGGGCTCCGTCCTCGCCTCCCAACGAGCG
ATCCCCGAGGAGAGCGCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAGAACCCGGGTGGCTGCGGCCCTTGCC
TCGCTTCCCGAGCGCGCGGCGGCTCGCAGCCTTGCCCTCTTGCTCGCCTTGAAAATGCGAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCTCGGACGATCTGCTCTCTCCCTCGCGAGGCCGAGGAGCGGCTCACGCTGGGAGGTCATCT
CTTAGGGGCGACACGCTCGAGCCACCCTCGAGACGGCCCTCTGAGAGATTTCTGTGAGAACAGCGGGCGAGACC
TGGTTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAGGTCGAAGAGTTTCATCGTGGAACA
TCTTGCAATTTCTGGACATTTGCTCTGATGTCAACCGAGTGGGCTGCTCCAAATATGGGCAGCACTGTCAAGAAATG
AGTTTCTCCCTCAAGACCTTCAAGAGGAAAGTCGAGGCTGGAGCTGCTGTCAAGAGGATCGGCATCTGTGCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATCCCTGAAATCGCAITTCAGAAGCGAGAGGGGGCCGCGCCCTGA
GGGAGAAATGTGCCACGGGTCATAATGATCGTGACAGATGGGAGACCTCAGGATCTCCGTGGCGAGGTTGGCTGCTA
AGGCAACGGGACACGGGTCCTTAATCTTTGCCATTTGGTGTGGGCCAGGTAGACTTCAACACCTTTGAAGTCATTTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTCTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTTC
AGAAGAAGTTGTGCACGGCCCAATGTGCGAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACGTTCTGAGGTGCAAAACAGGGCTACATTTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT
GTGCCATGGAGGACCAACAATGTGAGCAGCTCTGTGTGAATGTGCGGGCTCCTTCGTCTGCGAGTGCTACAGTG
GCTACGCGCTTGGCTGAGGATGGGAAGAGGTTGTGTGGCTGTGGACTACTGTGCTCTCAGAAAAACCGATGTGAAC
ATGAGTGTGTAATGCTGATGGCTCCTACCTTTGCCAGTGCCTGAAGGATTTGCTCTTAACCCAGATGAAAAAAC
CGTGCAACAGGATCAACTACTGTGCACTGAACAAAACGGGCTGTGAGCATGAGTGCCTCAACTGAGGAGAGAGCT
ACTACTGCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGAGGATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACAGGAGACCTCAAGACCTGTCTCCGGGTGGATTACTGCTGCTGAGTGACCATGGTTGTGAATCTCCT
GTGTCAACATGGACAGATCCTTTGCTGTGAGTGCTGTGAGGACACGCTGCTCCGAGCGATGGGAAGACGTTGT
CAAAATTTGACTCTTTGTGCTCTGGGGGACCAACGTTGTGAACATTCGTGTGAAGCAGTGAAGATTCGTTTGTGT
GCCATGCTTTGAAGTTATATATCTCCGTAAGATGGAAAAACCTCGAAGAGGAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGAGTGTGTGGAGGGATTCGGGCTCG
CTGAGTGTTGGGAACCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGGGAACACATTTGTGTTA
ATAATGGGAATTCATCACTTGCATAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT
GCATCTGAAGGCCCAATTGACCTGGCTTTGTGTATCGATGGATCCAAGATCTTGGAGAGAGAATTTGTAGGTCTG
TGAAGCATTTGTCACTGGAATTTAGATTTCTTGACAAATTCGCCCAAGGCCCTGAGTGGGCTGTCTCAAGT
ATCTCCACAGGTCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACATGAAAAGACCGGTGGCCCC
ACATGAAATTCATGGGAAGGCTCTATGACTGGCTGGCCCTGAAAACACATGTTTGAAGAGATTTTACCAAG
GAGAAGGGCCAGGCCCCCTTTCCACAGGCTGCCAGAGCAGCATTGTGTTCAACGACGAGCGGCTCAGGATG
ACGCTCTCCGAGTGGGCGAGTAAAGCCAAAGCCAAATGGTATCACTATGATGCTGTGGGTAGGAAGACCATTG
AGGAGGAACCTACAAGAGATTTGCTCTGAGGCCACAAACAGCATCTCTCTATGCTCCGAAGACTTCAGCACAATGG
ATGAGATAAGTGAAAAACTCAAGAAAGGCTATCTGTGAGGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCAG
CAGGGGAACTGCCAAAAACGGTCCACAGCCCAACAGAAATCTGAGCCAGTACCAATAATCCAAGACCTTACTTT
CCTGTTCTAAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAGACAACTCTTTTACGGTCTACACAAAAGCTTT
CCATTCAACAAAACCTTCAGGAAGCCCTTTGAAGAAAAACAGATCAATGCAAAATGTGAAAACCTTTAATGT
TCCAGAACCTTGCRAAACGAGAAGTAAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAAATCGCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTGATTCATTCAGGATTAACAAT
GAACGCAAGTCAGAGCCCCAAGCTCAGGCTATTGTTAAATCAATAATTTGTGTAAGTAAAAACATCAGTACTGA
GAAACCTGTTTGGCCACAGAACAAAGACAAAGATATACATACTTGTATTAATTTATTCAGGAAAAAATCCT
TCAGAATTTCAAGATGAATTTACAGGTGAGAATGAAATAGCTATCAAGAGATTTTGTAAATATACTGTGGACAC
AATCTGCTCTCTGCTCCTTGTGCTTAGTGTCGAATCTCACTTTGACTATACGATTAAGATTTGACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAATGTGTTTTTTGTACTGGACTTAACTTGATATATGATATGGATGATG
CATAAATCATAGGACATGTACTTTGTGGAACAAGTTGGATTTTTTATACAATATAAATTCACCATTCAG

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FIGURE 15

MEKMLAGCFLILGLQIVLLPAEARERSRGRSISRGRHARTHPTQALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEPSLTKFRKSEVERAV
KRMRLHSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDDGRPQDSVAEVAAKARD
TGILIFAIGVQGVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFPQKKLCTAHMCSTLEHN
CAHFICINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCBQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINRYCALNKPGE
EHECVNMEESEYCYCRHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSSEGLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCEGHVLRSDGKTCAKLDSALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCCELEGFRLLA
EDGKRCRRKDVCSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEELQBIASEPTNKHLFYAEDFSTMDIEISEKLLKGICEALEDSGGRQDS
PAGELPKTVQOPTSESEPTVINIQDLLSCSNFAVQHRHYLFPEEDNLLRSTQKLSHSTKPSGSP
BEKHDQCKCENLIMFQNLANEVRKLQRLBEMTQRMALENRLRY

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCAGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCTGTCGCTCCCGCGGCTGGCGCCCCTGACTCCGTCCTCCGGCCAGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAAATGGGACCCT
TTCTCTGTCACTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCTGTGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCGTGTATGGTGCTTCCCCAGAGTCAAGCTGGCTCTCTGGTAT**TGAT**GAC
CCCACCACTCATTTGGCTAAAGGATTGGGGTCTCTCCTTCTTATAAGGGTCACTCTTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGT CAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAACTAACATGAAATATGTGTTGTTTTCAATTGCAAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

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Signal peptide:

Transmembrane domain:

N-glycosylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

[illegible]

GGCACCACTGCGGCGACCGGCAATTGAAACGCCTCCCGCTCTCTAGTGGTTTTTCCACATTG
 TTGAATTGTTCTTCACTGACCAAAATTGCACCAAGACACCTGTCTCCCAAAATGCAAAATGTGA
 AATACCGAATGCGAATTAAGCTCGCTGTTATGCAACATGGGATTTTCAGGAAATGGTGTCAAA
 TTTGTGAAGATGATAATGAATGTGGAATATTAACTCAGTCTCGTGTGCGAAATGCTAATTGC
 ACTTAACACAGAAGGAATTATTATTGTGTATGTGTGCTACCTGGCTTCAGATCCAGCATACCA
 AGACAGGTTTATCATCTAATGATGGAACCGTCTGTATAGAAAAATGTGAATGCAAACTGCCATT
 TAGATAATGTCTGTATAGCTGCAAAATTATTAATAAACTTTAAACAAAATCAGATCCCAATAAA
 GAACCTGTGGCTTTTGTCTACAAGAAGTCTATAGAAATCTGTGACAGATCTTTCCACAAAG
 TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAC
 CTATCTCAGCCAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAAACCGTGAAT
 AATTTTGTTCAAAGGGATCATTTGTGATTTTGGGACAGTTACTCTGTGAATCATAGAGGAAC
 ACATCTTACAAAACCTCATGCAACCTGTTTGAACAGCTACTCTTAAGGATATCCAGAGACTTCC
 AAAAGACCACAGAGATTTGATACAAATTCAGACGGATATAGCTCTCAAGGTTTCTTTTTGTAT
 TCATATAACCATGAACATATTACTCTCATATGAATATGGATGGAGACTACATAAATATATT
 TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTGAGACTTGCAATTTTATATATATA
 AGAGATTGGTCTCTTGGCTTCATCATCTGACAACTCTTAATTGAAACCTCAAAATATTGAT
 AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCC
 ACCCACTATTATATGAATCTGAAAAAATAAATCTTACATTAACTGATCATGAAAGGTCACAGATA
 GGTATAGAGATGTGATGTGCATTTTGAAGTAATCTACCTGATACCATGAATGGCAGCTGTCT
 TCAGAGGGCTGTGAGCTGACATATCAAAATGAGACCCACACCTCATGCCCCTGTAATCACTT
 GACACAAATTTGCAATTTTGATGTCTCTCTGGTCTCTCCATTGGTATTAAAGATTATAAATTC
 TTACAAGGATCACTCAACTAGGAATAAATTTTCACTGATTTGCTCTGCCATAGCATTTT
 ACCTTCTGGTTCCTGAGTGAAATTCAAAGCAGGACCAACAAATTCACAAAATCTTTGCTGT
 FAGCCTATTCTTCTGCTGAACCTTGTTTTCTTGTGGGATCAATACAAATCAATAATAGCTCT
 TCTGTTCAATCATTTGCCGGACTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGC
 ATTTGAAGGCATACATCTCTCATCTATTGTTGTGGGTGCATCATCAACAAGGATTTTGTGCA
 CAGAAGATTTTTATATCTTTGGCTATCTAAGCCACCGCTGGTATGTTGAATTTTGGCAGCAG
 TAGGATACAGATATTATGGGCACCAACCAAGTATGTTGGCTTAGCACGAAACAACTTTTAT
 TGGAGTTTTTATAGGACCATGCCATTAATCATTTCTGTTAATCTTTGGCTTTTGGGATGATC
 CATATACAAAAGTTTTTCTGCACACTCAGGGTTGAAACCAAGAGTTAGTTGCTTTTGAGAAC
 TAAAGTCTTGTCGAAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACTGGATCTTT
 GGGGTTCTCCATGTTGTGCACGCACTGAGTGGTTACAGTTACCTCTTCACAGTCAGCAATGCT
 TTTCCAGGGGATGTCATTTTTTATTTCTGTGTGTTTTATCTAGAAAAGATTCAAGAAGAAAT
 ATTCACAGATTGTTCAAAAGTGTCCCTCGTTGTTTGGATGTTTAAAGTTAAACATAGAGATG
 GTGATATATTAACCTGCACAAAAATAAAAAATCCAAGCTGTGATGACCAATGTTATAAAA
 TGACTCATCAAAATATCCAATTATTAACTACTAGACAAAAAGTATTTTAAATCAGTTTTTCT
 GTTTATGCTATAGGAACGTGTAGATAATTAAGGTAAAAATATGATCATATAGATATACTATGT
 TTTTCTATGTGAATAGTTCTGTCAAAAATAGTATGTCAGATATTTGGAAGATAAATGGTTT
 CTCAGGAGTGATATCACTGCACCTGCGGAGAAAGATTTTCTTTTAAACACGAGAAGTATAGAA
 TGTCTCTGAAGGAACCACTCGCTTGATATTCTGTGACTCGTGTGCTTTGAAACTATGCC
 CCTACACCTCGGTAAATGAGCTCCATTACAGAAAGTGAAACATAAGAGAAATGAAGGGGCAGA
 ATATCAACACAGTGAAGAGGGAATGATAAGATGTATTTGAAATGAACCTGTTTTTCTGTAGC
 TAGCTGAGAAATTTGTGACATTAATAAAGAATGAAGAACACATTTTACATTTTGTGTGAA
 TTGTTCTGAACCTTAAATGTCCAATAAAACAACTTAGACTCTGTTTGTCAAAATGTTTCTT
 TTTCTTAATATTCTAAAAAATAAAAAAGGTTTACCTCCACAAATTGAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 19

MKRLPLL VV FSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNV CIAA
NINKTLTKIRSIKEPVAL LQEVYRNSVTDLSPTDIITYIEILAESS SLLGYKNNTISAKDTL
SNSLTLEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFOKTEFDT
NSTDIALKVFFFD SYNMKHIHPHMNMMDGDYINIFPKRKAAYDSNGNVAVAFLYYK SIGP LLS
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTD RYRSLCAF
WNYSPDTMNGSWSSEGC ELYSNETH TSCRCNHLTHFAILMSSGPSIGIKDY NILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLF LAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAAFAWMCIEG IHLVYLVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNFIW SFIGPA CLIIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGV LVHVHASVVTAYLFTVSNAFQGMFI FLFLCVLSRKIQE EYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAAGAGTCATATCTTCAGTAATTTCACTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCTCCGAAACCCGGCCG
CTAAGCGAGGCTCTCTCTCCCGCAGATCCGAACGGCTGGGGCGGGGTCACCCCGGCTGGGA
CAAGAAGCCCGCCGCTGCTTGCCTCCCGGCCCGGGGAGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAGAGAAATGCTCGGG
TGCTTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGGCCGGAG
CCGCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCTTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCTCTTGCTGGCGGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGTGGACTGCGCGCGGGG
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACACAGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCGAGGAGCGCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTCTCTTCCGCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTACCGGACTGGAGGCGGTGAGGAGTCCAGCTTTGAGAAGTAACT
GAGACCATGCCCCGGCCCTCTTCACTGTGCCAGGGGCTGTGGTACCTGACGCGTGGGGGACG
TGCTTCTACAAGACAGTCTGAGTCCAGTTCGTTTAGCTTTAGGAAGAAACATCTAGAA
GTGTACATATTAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGTGCTGGGCCCCCATCTGTCTCCCTCGA
GGTTGTGCGACAAGCTGTGCACTGTCTCAGTTCTGCTGAATACTCCATCGATGGGGAAC
TCACTTCTTTGGAAAAATTTATGTCAAGCTGAAATTTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACACAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTTCCC
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAAATCTGTCTCCGGTGTCACTGTG
TTCATCTCCCAGCCCCACGCCCCCTGCCCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAGAGAAAGAT
TTGAAGACCCCAAGTCTTGTAATAAATTTGCTGTGTGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCGCAGCACTTGGTTTTTCCAACATGATATTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAATAATGGAGTTTGTGTTGT

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FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

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FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGCGCAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCATATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACCTGGAAT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGATGCTAT
GCTCAGAGGAAAGGCTACTTTTTCAAAGAAACCTCCTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGCGGGCGGATCACGAGGTGAGGAGTTCTAGACAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAAACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAAATCTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

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FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQBAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIIRLLENPRLGQSQT
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCCTTTTCAAGACGAGGAAGAGGAGGAGAAAAGAG
 AAAGAAGAGGAAGATGTTGGGCAACATTATTATTAACATGCTCCACAGCCCGGACCCCTGGCAT
 CATGCTGCTATTCTCGAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
 ATGAATTACTCAATCTCTCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
 TTATATCATTAAAGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGCAATG
 CAATTGTGGCACTGGCCTTATTTAGTGAAGAAAACTTTGTGGTTCTATGGCATTATCA
 TTTGACAAATGCAAGCATCTTCTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
 TGGAACTCCTTAAGGGCCCATACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGGCCAT
 CCGAATTCATGTGCTACTTGGCCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAATCAGGCCCTTGGTTTACACCCAGATCCATTAT
 ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
 AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATTATGCAAAAATTGAATACTCCACAG
 ACTTTCCAGTAAACCTTACTGGCCCTGGATTATCTCAAAACAATTTATCTTCAGTACCAAT
 ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA
 ACTGCCCTGAAAAATGTCTGTCGGAACCTGAGCAACTTACAGAAGACTCTATATTAATCACAAC
 TGCTTTCTACAATTTCACTGGAGCCTTTATTGGCCTACAATAATCTTCTTCGACTTCATCTC
 AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAGAGAT
 TCTGCTGATTGGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA
 ATCTTGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAATACCAGATAACGCCTTGGTT
 GGACTGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAACTCTATTAATAGAA
 TACGAAGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACACCCTAGATTGTCTTACATTACCCCAATGCATTTTCAGACTCCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATTGAGTCTCTG
 CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCACTCGTGTG
 GATGAACATGAACAAAAACCAATTCGATTTCATGGAGCCAGATTCACTGTTTTCGCTGGACC
 CACCTGAATTCGAAGTTCAGAAATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAATTTGT
 CTCCCCTTATAGTCTCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
 TTCCCTTTCAGTGTAGAGCTACTGCAGAACCACAGCCCTGAAATCTACTGGATAACACCTTCTG
 GTCAAAACTCTTGCCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
 GATATAAATGGCGTAACTCCCAAAGAAGGGGTTTATATACCTGTATAGCAACTAACCTAGT
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCAAAGATAACAAATG
 GCTCTTTGAATATTTAAATAAGAGATATTTCAGGCCAATTCAGTTTGTGGTGTCTTGAAAGCA
 AGTTCTAAAATTTCTCAATCTAGTGTTAATGGACAGCCTTTGTCAAGACTGAAAAATTCCTCA
 TGCTGCGCAAGTGCTCGAATACCATTCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
 CATCAACTGAGTATAAAATTTGTATTGATATCCACCATTCTACAGAAAAACAGAAAAAAA
 TGTGTAATGTCCACCACCAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
 CACAACACTTATGGCCCTGTCTTGGAGGCCCTTCTGGGGATTTTGGTGTGATATGTCTTATCA
 GCTGCTCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
 AAACCAACCTTTGCAATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAGCAGGAAA
 AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCAAGGAAACCTTCAAAAATGAAC

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FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQIILLQTNNAIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTLEPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLLENLESISFYDNRL
IKVPVHALQKVVNLFKLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHNSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPEPFQGNVRQVHFRDMMEICPLIAPESFPPSNLNV
EAGSVVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDKFYVHSEGLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPFMNCDGGHSYVRNYLQKPTFALGELYPLPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

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FIGURE 27

CCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCAATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTGTGTTCTTA
TGATACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAACGTCCTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTACCA
TGTTTGGCTGGTTCCTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCTATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCACTTTTTTTGAATTATGCCACTGCTGAACCTTTTACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAGCAAATAAAAGCTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 28

MNLVDLWLTRSLMCLLLQSFVLMILCFHSASMC PKGCLC SSSGGLNVTC SNANLKEI PRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGV AETLQTLDSLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHN VICKTSVLDEHAGRPFLL
NAANDADLCNL PKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKS LPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTGAGGCTCGGCCACGGGCTGCCGCCCGCTGCGAGTGCTCGGCCCAGG
ACCGGCTGTGCTGTGCCACCCCAAGTGCTTTGTGGCAGTCCCCGAGGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGACGCAACCGCTGAAGCTCATC
CCGCTAGGGCTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAAGT
CGTTATCCTACTGGACTACATGTTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCCTCAACAGCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGCGCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCTACACCCCATCA
GCACCATTTGAGGGCTCCATGTTGTCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTTCCGCGGCCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCATCTCGGTGGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTGTTCCTCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCCACTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCACGAGGTGTTTGTGGACGAGGCGCCACACGGTGACGTTT
GTGTGCGGGCCGATGGCGACCCGCCGCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCGCCCACTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCGCCGGGCGAGGAGAGGCCAACAGCACCCGCGCACTG
TGCCCTTCCCTTTCGACATCAAGACCTCATCATCGCCACCCATGGGCTTTCATCTCTTTC
CTGGGCGCTGCTCTCTTCTGCTGCTGCTGCTGTTTCTCTGGAGCGGGGCAAGGGCAACAC
AAAGCACAACTCGAGATCGAGTATGTGCCCGAAAGTCGGACCGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGCGGGGGGCGAGGACCCCCG
GGCGGCGGGCAGGGGAAGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCTTCTACACAGTCTCTTTCTCCCTCCGCGCTCCGTCCTCTGTCGCCCGCCG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCGACAGCTGGGGACCCCA
CCTACACAGGGGATGACAGACTGGAGTTGAAAGCCGACGAAACCGACACGCGCGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTCATTAATTATGGATTTT
TATGAAACTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLLGKNRIKTLNQDEFASFPHLEEELELNENIVSAVEPGAFFNNLFLNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGGLNSLEQLTLEKCNLTISIPTALSHLHGLIVLRLRHLNINAI RDYSFKRLYLKVL EISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSM LHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLTEESVFHSGVGNLETLLILDSNPLA
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDMPAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCAGCCCCCGGGATTACGGCTCGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTG
TGTTTCGCCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGTGGTGGCACCGTGGTGTCTCAAGTGCCAAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGTCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAAATCGAATTACGTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGTCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGTCTAGGAATCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCACTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGCGCAGCATCGTGTCTCTGTGAACCATGAATCTCTAAAGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCTCTAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCTCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTTCATTGTCTTCTCTGCTG
CTCATCATGTCTCATCTTCTTGCCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGTCTCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCTCTGC
GCCCCCAGGGGCCCTGTGGGGACTGTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCAACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGAATGGGGAGGGAGGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

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FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTCTCCTTTCTGG
 CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
 TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATCTGCTGCTTTGGATCTCTGT
 GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAACGTTACAGGGGACGTTTGCAAGAGAGAAGA
 TCTGTTCTCGAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
 AGTCTGCAGCGTTTCACTGCCCGGACTTCCAGTTTTACCATTTATTTCTGCACTGGCAATTC
 CCTCACTCGACTTTTCCCTAATGAGTTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
 AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAGAAG
 CTGCACATCAACAACAACAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGCTGGACGA
 TCTGGAATATCTCCAGGCTGATTTTAATTATTACGAGATATAGACCCGGGGGCTTCCAGG
 ACTTGAAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC
 GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAACCGTGCC
 CTATGAGGAGGTCTTGAGCAAATCCCTGGTATTGCGGAGATCTCGCTAGAGGATAACCTT
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGAAAAACATTCCCAAGATGCC
 CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGGTAAGACCTCAATGAAAC
 CACCGAACAGGACTTGTGCTTTTGA AAAACCGAGTGGATTCTAGTCTCCCGCGCCCCCTG
 CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAATCTCTTTCAAGACAAATGGGCAAGAG
 GATCATGCCACACCAGGCTCTGCTCCAAACGGAGGTACAAAGATCCAGGCCAATCGGAGCAT
 CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCTTAGCTAAACA
 GTTTACCCCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTCCGGGTTTAAAGATGAAC
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTTAAAGTGACGGA
 GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAAATCGCACTTTGTGGATTACAAGA
 ACCTCATCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG
 AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTCTCCGGGA
 GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGTCA
 TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAAACCTG
 CTGAGGTCCCTGCCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTAAACTCAGCTGCACAA
 CAATTACTTCTATACCTCCCGGTGGCAGGGGTGCTGGACAGTTAACCTCCATCATCCAGA
 TAGACCTCCACGGAACCCCTGGGAGTGTCTCTGCACAAATTGTCCTTCCAGTGGCGCA
 GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGCTGAACCTCTT
 TGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCTCAGCTGTACGCTAGGATCT
 CGGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGACGCACTCC
 AACTCCTACCTAGACACAGCAGGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
 GTTTGTCACTCCGCCCTTACCCTGGTGGGCACTGCTCGTGTATTATCTGAGGAACCGCAAGC
 GGTCGAAGAGACGAGATGGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT
 GACTCTTCTTACTGGCAACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
 TGGCTCTCATCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGCGAGGGGAAGGCG
 ATACATCTTCCCCACCGCAGGCACCCCGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
 CCATCAGCTAGTGGGCATAGTAGATAAATAACTGTGAGCTCGCACACCCGAAAGGGGCT
 GACCCCTTACTTAGCTCCTCTTGAACAAAGAGCAGACTGGGAGAGCTGGGAGAGCGCA
 GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTGACAGAAAGCCGACGACCCCTGTCTGGAAG
 AACTGACAGTGCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCGCGGTTCTATAC
 ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
 CCCCCTGATGGCTCCTGTGGCTACGAGGGATGGGAGTTGCACGAAGGCATGAATGTAT
 TGTAAATAAGTAACCTTGACTTCTGAC

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FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLPNEFANFYNVAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLRLDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLTPYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNQGEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIAIATGSSRNKPLANS LPCPGGCSCDHI PGSG LKMNCNNRNVSS LADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAIQLILPGTFNAMPKLRIILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPOLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFTSAFTVVGMLVFIILNRKRKRDRDANSSASEINSLQTVCDDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGTACCCCAAGAATAAATCTCAGGGC
 TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAATCTTTGGC
 CGCTGGGGCCCGCGGGGGATTTCTGGCAGTTGGGGGTCCTCGGGAGCGAGGGCGGAGGGG
 AAGGGAGGGGAACCGGGTTGGGGAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
 AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCTCAG
 AGAATGAGGCCGGCGTTTCGCCCTGTGCTCTCTGCGCAGGCGCTCTGGCCCGGGCCGGGCGG
 CGCGGAACACCCCACTGCCGACCGTGTCTGGCTGCTCGGCCCTCGGGGGCTGTCTACAGCCTGC
 ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCTGCATCTCTGCGAGGTGGGGCGCTC
 AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTCTGCGGGCAGGCCCAGG
 GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCTCACT
 GCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGCGGTCTC
 GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTGACCCGCGCGAGATGCGC
 GGTACTCCAGGCCACCGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
 GCGCCAACGGCTACCTGTGCAAGTACCAAGTTTGAGGTCCTTGTCCTGCGCCGCGCCCGGG
 GCGCGCTCTAATTTAGACTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
 TCCACCTGGGACCGAGGTGAGTGCGCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTTGCA
 TCGCGGACGAAATCGCGCTCGCTGGGACAAATCTCGGGCGATGTGTTGTGTCCTTGCCCC
 GGGAGGTACCTCCGTGTGGCAAAATGCGCAGAGCTCCCTAACTGCTAGACACTTTGGGAGG
 CTTTTCCTCGCAATGTGCTACGGGCTTCGAGCTGGGGAAGGACCGCCGCTCTTGTTGTGACCA
 GTGGGGAAGGACAGCCGACCTTGGGGGACCGGGGTGCCACCAAGGCGCCCGCGGCCACT
 GCAACCAGCCCCGTGCCGACAGAGAATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
 ACCACTTTGCCCTGAACAAGACAAATTCAGTAACATCTATTCTGAGATTCTCGATGGGGAT
 CACAGAGCAGATGTCTACCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
 CCATCAGGGAGCGTGATTTCCAAAGTTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTT
 CGACTCTCTCTGCGCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGTTGGTGATCT
 TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTTACGAAAGCCCTCTTCCAGCCA
 AGGAAGGAGTCTATGGGCCCGCGGCCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
 CAGTTCTGCACATTTGCACAAACAAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
 CAGAGGGTGCCCTTGTGCGCGAGTCCCCTCTTGCTCTAGTGATGCATAGGGAAACAGGGGA
 CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC
 TTGTGTAATGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTTCCCTTTACTCCACTGAG
 GAGCTAAATCAGAAGTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCTTTAGGA
 TGGTGATACTGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA
 TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAACAAATAGAACACAATATAATTTACA
 TTAATAAATAATTTCTACAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
 ATTGTTTCAAAATCCAGGGAATAAATAAATAAATAAAGGATTGTTGAT

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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIAD EIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI PVSTAVVVVLVILTM TVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

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FIGURE 37

CGGACGCGTGGGATT CAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGGCGCCCCGCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCTGGGGTGCAAACCCGAGCGCTTACGCTGCCATGA
GGGGCGCGAAACCGCTGGGCGCCACTCTGCCTGTGTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTTCTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCTCCAAATAGCAAATGTACTTGGAAATCA
CAGTTCCTCCGAAGGAAAAGTAGTCTGTTCTCAATTTCCGATT CATAGACCTCGAGAGTGACAAC
CTGTGCCGTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGATTACCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATT CAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATT CAGGCCAAAA
AAACTGCCTACAACCTACAGAACAGCCTGTCAACCACCAATTCCCTGTAACCA CGGGTTTAAA
ACCCACCGTGGCCCTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCGGCACTGTTATCAAAACCATCACTCGCGATGGGAGTTTG
CAGGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATT CAGCAGGCGGG
CAAGAACATGAGTGGCAGGCTGACTGTCTGTCTGCAAGCAGTGCCCTCTCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCCTTAAAAAATAAGCAATG
TTAA CAGTGAACGTGTGCCATTTAAGCTGTATTCTGCCATTGACCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAAATACTTTATAAAATTACATATTCTGAAAGAGGATTCGAAAAGATGG
GACTGGTTGACTCTTACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCCTGTGTGAGAGGACGAGCTATCTGATTGGAACCTGCCGACTTATGTCGGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTATAGT
GTTATTGTTTTCAACCTTCAAGCCTTGCCCTGAGGTGTACAATCTGTCTTGCGTTTCTA
AATCAATGCTTAATAAAATATTTTTTAAAGGAAAAAAAAAAAA

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FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPNSKCTWK
ITVPEGKVVLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMPSAAEFNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQOKCRRTGTLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQOQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

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FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGGTGGGGCGGTGCGTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCAGCCTGGGTAAGATGCGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCTATACCTG
CCGGGGACTGGTTGACAGCTTTAACAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAAATTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAACAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTGT
TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAAGTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCGTGTGAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAAACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCTAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACTGTAGGACCTCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCC
TCCTGTCTGGACACTCAGGACAGCTTGGTTTATTTTGGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTATCCAGGCCCGGGCAGACAAGGCCCTTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGGACTGGCAGGCTTCAATGTGTGA
ATTTCAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCTTACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGTGCATGCTGCCAGTTCCTGT
TCTGTGTTTACCACATCCCCACCCCAATTGCCACTTATTATTATCTCAGGAATAAAGA
AAGGCTCTTGAAAGTTAAAAAATAAAAAAAAAAAAAAAAAA

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FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPPIWLQSPSPPPQSSPPPPQHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLELSEELVESWWFHKQ
QEAPDLFWLCSDSLKLCPPAGTFGSPCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPPEESNCLQCKKGWALHHLKCVDDIDE
CGTEGANCGADQFCVNTESGYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICABGYKQMEGICVKEQIPESAGFFSEMTEDELVLQQMFFG
IICALATLAAKGLDVFTAIFIGAVAAMTGYWLSERSDRVLEGGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCTCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCAATGCAGCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTTGCCCTTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCTTGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGTCCCGCGGAAAGAGGTTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTCTGGCGTTGGAGGGCCAGCACACACCTGCTGGTGTTTCGG
CATGGAGCAGCGGTGCCGCCCAACAGCGAGCTGGTGACGGCCGTGCTGCGGCTCTTCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCC CGCGCAGCGCCCGGGCC
CGGGTGACCGTTCGAGTGGCTGCGCTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTACAGGTGTCGGTGACAGAG
GAGCATCTGGGCCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGCCGAGAAGTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGAGGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCTTCGACAGTGCATCGCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGACAGAA
GTGCAGCTGTGCCTCGGATGGTGCGCTCGTGCCAAGGAGGCTCCAGCCATTAGGGCCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACCTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTATTATTCACTGCACATATTTCTAAGCACTTACAT
GTGGAGATACTGTAACTGAGGGCAGAAAGCCCCANTGTGTGCTATTGTTTACTTGTCTGTGCTC
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAACATGAATAAAACATTTTATTCT
AAAA

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Signal sequence:

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGAGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTTGGGCAGTGTTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGTCTATAATAACAAGATCAGACTTCCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCTGCCTTCAGCAACTCTTCCTATGTCTCT
GAATCCCAACACGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTATCTGTGGCAGCGCTCCTTGTAAACCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCGTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC
TACACCCCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTAA
GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTCTCGGGCTCTTCTCTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAATGGGAGCTCTGTGTGTGGAGAGCATAGTAAATTTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCGAGGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTTCGGGATCAGCCTGACCA
ACATGGAGAAACCTTACTGGAAATACAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW
KFDQGDITRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYYTCMVSEBGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTGMTSNAVRMEAVERNVGVIVAAVLVTLLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCAGGCCGCGAGGCCCGAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAAGTGCGTTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGACTGCGAGCGATGGCAGCGATGAGGAGAGTGCGAGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCCTGACCGGCGTCA
GTGACTGCTCTGGGGGAAGTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCTCTCTGTCGGGAATGCCACATCCTC
CTCTGCGGAGACCACTCTGGAAGCCCAACTGCCCTATGGGGTTATTGCAGCTGCTCGGTTGC
TCAGTGCAAGCCTGGTCACCGCCACCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCCTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAAGTGG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

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FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFKQCR
TSGLCVPLTWRCRDRLDCSDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

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FIGURE 47

CCCACGCTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCTGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTCCAGGCAACCAAGTGTGCTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCAGGGGAGTCAGAACTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAA
GTCGTGATTACCTCCAGGTGCCAAGAGAGCACCACCCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACAGCCCAAGGCATCCATCATGCCCACTGGGT
GTTGTTCTTAAGAACTGATTGATTAAAAAATTCCCAAAGTGTCTGAAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTCTCTTGGTTTTAGACAAATGTAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRL LAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPSPRSSSDPDFVVVD
GVFVMLPSYDEAVSGGLSALGPGYMASVGQGCPLFVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFRLN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

090283.071001

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGC GTGCGTCCGTCCGTCCGTGGCCCTAGAGA
TGCTGCTGCCGCGGTTCAGTTGTGCGGCACGCCTCTGCCGCGCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTCTGGGGGGCGCACCCGAGTCTGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGCAGCGGTGCGCTGCTGAGTGGC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGAGCTGATGGCAGCATAT
CACAAATTAGGAACTGGTATGTGGATGAGCCGTCTCGCGCAGCGAGGTCTGCGTGGTTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCCCTACATGTTCCAGTGGAATGATGA
CCGGTGC AACATGAAGAACAAATTTTCAATTTGCAAAATATTCTGATGAGAAACAGCAGTTCCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTTCCCTTCTCCTCCTCTGTGGTCAACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTTATTCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGTTGGACCCCCACGTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAAGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAACACACCTCTGTTTCCCTTGCTCTATACAG
CAGCATATTATCATACAGACAGAAAAATCCAGAACTCTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

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FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD F WIGLR RREEKQSNSTACQDL
YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREAA NLAYILIPS IPLL LLLLV
VTTVCWWVICRKRKREQPDSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETR PDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESG GFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

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FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGTCTGAAGGGCTGGATGTACGC
ATCCGAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCTCTCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTTACCACTATGATCACTGGTGT
GTTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGTGAAGTTGAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCGACTATTAGAGGTCCCAACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCTACTAACATTTTTCGGAATCTG
GAGTCCACCCGTGTTTGTCTGGCTGGGCTTTTCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCTCTCT
GGACAAAGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAAAGAGAGCTGTGGACACATCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCTCCACATCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCACTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAAATAAGTGCCCTTTATACAATG

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FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRVALAELQEADGQCPVDRSLLKLMVQVVRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQMQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQCKE
GPILIHTEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKVKVDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFAIRMIQRAVDTSLYILPKEDRESLQMAVGPFPHILES
NLLKAMDSATAPDKIRKILYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSIVTTLSPKYLALCSQTQVMEVGNNE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

0902853-071001

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCAACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGTGTACGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCACTGGTATACCGTGTGC CAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG
TGTGCCGCGAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTGTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTGTAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCATTGTCTCTGTTTCTCTGAAGAACTCTGACAAAAATACAGATTTTGGTACTGAAAGAGA
TCTTAGAGGAACGGAATTTTAAAGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

0902853.07103

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCGRVEVEQKQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEEDAGASC
ENPESSSFSPVPEGVRLADGPGHCKGRVEVKHQWYTVCCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

090253.071001

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACTCCACAGCCATCCTGCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCTCTTTCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTCTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGTGAGACTTTAATGGAGATTTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATGCAGCTTATAATGGTTAC

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FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALBELIRELTASHATKVQTHKPVLVTFDLTDSGAIVAAAAILQCFGYVDIL
VNNAGISYRGTIMDTTVDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGMKI
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDDTT
AQGRSPVEVAQDVLAAGVKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

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FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTCTAA
GAGGAGAAAATCAGTCACCGCGCAAATCGTGTCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCATGAATTTGCTAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTTCCTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTGTCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTTAATTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAGCACCTAGTTTTCTGAAAACGATTACCAGGTTTAGGTTGATGTCTATCTA
ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCATTCTTCAATA
TCATTTTGGAGGCTTGGCAGTCTTCATTACTACCACTGTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTTGCAA
AATTGTAACATAACCGTTTATTTAACATATATTTTATTTTGTATGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACCTCTCAATGGGTAGGTTTC
ATCTTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

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FIGURE 58

MKFLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

090265.071001

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTGGATGCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTCTGGTTC
TTCACAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCAAGTAACATGA
CCTTGGCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTCAGTTTTCCAGATATTTCTGAATATAAAATA
ATGACTTTTATGTCACTGGGAGTCTTATGCAGGGAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAAGTGGTTTGGGCCCTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGAG
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACCTGGACATCATCGTGGCAGCTGCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCCGAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCAAAAGAGAACAT
CAGAGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGAGATGTTTACTACAAAATTACATGAGTACATGAGTAAGAAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAAAGTGCACTTG
TAACAAACAAGCTGTAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAGTAAAAA

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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGSGQLFLTPYIEAGKIQKGRELSL
VGPFPGNLNKS YAGFLT VNKT YNSNLF FWFPPAQIQPEDAPVVLWLQGGPGSSMFGLFVEH
GPYVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F
F Q I F P E Y K N N D F Y V T G E S Y A G K Y V P A I A H L I H S L N P V R E V K I N L N G I A I G D G Y S D P E S I I G G
Y A E F L Y Q I G L L D E K Q K Y F Q K Q C H E C I E H I R K Q N W F E A F E I L D K L L D G D L T S D P S Y F Q N V T G
C S N Y N F L R C T E P E D Q L Y Y V K F L S L P E V R Q A I H V G N Q T F N D G T I V E K Y L R E D T V Q S V K P W L T
E I M N N Y K V L I Y N G Q L D I I V A A A L T E R S L M G M D N K G S Q E Y K A E K K V W K I F K S D S E V A G Y I R Q
A G D F H Q V I I R G G G H I L P Y D Q P L R A F D M I N R F I Y G K G W D P Y V G

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
 TTTTCCTTTTCTTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
 GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
 CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
 TCTAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
 CTGGGGGAGGGCCTGCCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
 AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTGTCTCTAATATCAAAATTGACTGGCTGGG
 TGAACCTTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGCCAGAAA
 TAGAGATGCTTTGTAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
 GACCAAAATAGATAACAGGATTCCCTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA
 GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCTCTGGGTC
 AGGCCAGCCTCTTTGCTCTCCCGAAATTATTTTGGTCTGACCCTCTGCCCTGTGTGTTTT
 GCAGAAATCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACAGGAGCCGTCT
 CCTCACCGCCGCCCTCTCAGCATGGAAACAGAGGCAGCCCTGGGCCCGGGCCCTGGAGGTGG
 ACAGCCGCTCTGTGCTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
 ATGCCCTCAGTTCAGCACTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
 CCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGGCA
 ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAAGTCTCGTTACCCG
 CCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCCTCAACCAAAATGTCAACAAGCTGCT
 CATCATTGACTACTCTGAGAACCCTGCTGCGCTGTGGGAGCCTCTACCAGGGGGTCTGCA
 AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCAACAAGAGGAGCACTAC
 CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
 TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
 GCCGGAAGCTGCCCGAGACCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
 TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCCATTTTGACAT
 CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
 CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
 CTCTGCAAGGATGACCCCAAGTTCCTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
 CGGGGTGGAATACCGCTCTCTGAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
 AGGCCCTCAATATCACCAAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAGGGCGAGAAG
 CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT
 GCAGATCAAGGAGCGCCTGTCAGTCTGCTACCAAGGCGAGGGCAACTGGAGCTCAACTGGC
 TGCTGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA
 CTGGACATCAACAGCCCTCGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
 CAGCAGGGACCGCATGACCTCTGTGGCTCTCTACGTTTACAACCGGTACAGCGGTGATTTTGG
 TGGGAGCTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTTCAAGTGTCCAATGCC
 ATTCACTCTCTCAGCAAAGAGTCCCTCTTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
 GCAACTTTATTTCTTGGGGAACAAGGTTGAATGGGGAGGTAAGAGGGGTTAATTTTGTG
 ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCACTTGGGTATGTAAGGAATCAAGCGTA
 TTTCAATATTTCCAACTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

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FIGURE 62

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLTLTAAPLSMEQRQPWP
RALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFIIVPEPSHKKEHYLSSVNKTGMTYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSRRLPRDESSAMLDYELHSDFFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPDDSALCAFPPIRAINLQIKERLQSCYQEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTGSKGLKKVRVYEFRCNSNAIHLLSKESLLEGSYWWRFNRYQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 63

AGGCTCCCCGCGCGGCTGAGTGCAGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAAACGCGCATGACCA
 CGTGGAGCCTCCGCGGAGGCGCGGCCGACGCTGGGACTCTGTCTGTGTCTGTGGGCTCTCTGTGTCTCT
 GCAGGCTGGAGCTGGAGCACCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGAGGCTCGAGGCCAAGGGCTGGA
 ACTTCACTGTCTGAGGAGTTCCACCTTCTGGATCTCTGGGGGCTCCATCCACATATTTCCGTGTGCCAGGGAGTACT
 GGAGGGACCGCTCTGAAGATGAAGGCTGTGGCTTGAACACCTTCCACCACTATGTTTCCGTGGAACTGTGATG
 AGCCAGAAAGAGGCAAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCGCTTGTCTGTATGGCCGCGAGAGATCG
 GGCCTGGGGTGAATTCCTGCTCCAGGCCCTCATCTGTCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC
 TCCAAGACCTTGGCATGGGCTGAGGACAACTTACAAGGGCTTACCGAAGCAGTGGACCTTTATTTTGACCACT
 TGATGTCCAAGGTTGGTCCACTCCAGTACAAGCGTGGGGGACCTATCATTTGCCGTGAGGTGGAGAAATGAATATG
 GTTCTCTATAATAAGACCCCGCATACATGCCCTACGTCAGAAGGCATCGAGGACCCGTGGCATTTGTGGAACTGC
 TCTGTACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGAGATTGTGGCCACCATCAACTTGTGAGT
 CAACACA CGAGCTGCAGCTACTGACCACCTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGTGAGGT
 ACTGGACGGGGTGGTTGTACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT
 CTGCCATTGTGGACGCGCGCTCTCTCATCAACCTCTACATGTTCCACGGAGGCACCAACTTGTGGCTTCATGAATG
 GAGCCATGCACCTTCCATGACTACAAGTCAGATGTCAACGACTATGACTATGATGCTGTGCTGACAGAAGCGCGG
 ATTACACGSCCAAGTACATGAAGCTTCGAGACTTCTCGGCTCCATCTCAGGCGATCCCTCTCCCTCCCCACCTG
 ACCTTCTTCCCAAGTACCGGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGGGGACGCCCTCAAGTACC
 TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
 TCGGGTACATTTCTCTATGAGACACGATCACCTCGTCTGGCATCTCTCAGTGGCCACGTGTCATGATCGGGGGCAGG
 TGTTTGTGAACAAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATGCTGTCTGCTGATCGAGGCTG
 ACACCGTGTGAGGATTCTGTGAGAAATCGTGGCGAGTCAACTATGGGGAGAAATATTGATGACCAAGCCAAAG
 GCTTAATTTGAAATCTCTATCTGAATGATTCACCCCTGAAAACTTCAGAATCTATAGGATATGAAAGAAGA
 GCTTTCTCAGAGGTTCCGCTGGAACAATGNGNPTCCCTCCAGAAACCCCACTTACCTGCTGCTTCTTCTTGG
 GTAGCTTTGTCATCAGCTCAGCGCTGTGTGACACCTTTCTGAAGCTGGAGGGCTTGGGAGAGGGGGTGTATTCA
 TCAATGGCCAGAACCTTGAGCTTACTGTGAACATTTGACCCCAAGAACCCCACTTACCTCCAGTCTCCCTGTGGA
 CGAGCGGAATCAACAGCTATCGCTTTTGGAGAGACGATGGCGGGCTTGCATTACAGTTTCAGGAAACCCCCC
 ACCTGGGCGAGGAACAGTACATTAAAGTGAAGCGGTGGCACCCCTCTCTGCTGGTCCAGTGGGAGACTGCCGCTC
 CTCTTGACCTTGAAGCGCTGGTGTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACTCTCAGGG
 ACTGGGGGCTCAGTCTGCCCCCTGTCTCAGCTCAAAACCTTAAGCCTCGCAGGAAAGGTTGGGATGGCTCTGGGCT
 TGGCTTTGTGTATGATGGCTTCTCAGACCCCTGCTCTTGTGCGGAGGCTGTGGGCTGTCTCTAGGTTGGGAGC
 AGCTAATCAGATCGCCACGCTTTGGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGCACCGGACGTCAACAGCC
 TGCAGCATCTGTGGACTCAGGCGTGTCTTTGTGCTGTTCTGGGAGGCTTGGCCATATCCCTCATGGCCCCAT
 TTTATCCCCGAAATCTTGGGTGTGTACCAAGTGTAGAGGTTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
 CTTCTTCAACACCTCTGAGCCTTCTTGGGATTCTGGAAGGAACTCGGCTGAGAAACATGTGACTTCCCTT
 TCCCTTCCCATCTCGTGTCTTCCACAGGGTGACAGGCTGGGCTGGGAGAAAAGAAATCTCCTCAGCCTCGCTTCC
 CAAGTTAGCAGGTGTCTCTGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
 CATCCAGGGAGGAGGACAGAAGGCCAGCTCACTGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCC
 AGGGAGGAGGACAGAAGGCCAGCTCACTGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCCAGGGA
 GGAGGACAGAAGGCCAGCTCACTGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCCAGGGAGGAGG
 ACAGAAGGCCAGCTCAGTGGCCCCCTCCACCCCCACGCCGACAGCAGGGGGCAGAGCAGCCCTCTCTC
 GAAGTGTGCCAAGTCCGCAATTGAGCCTTGTCTGGGGCCAGGCCAACCTGCTTGGGCTCACTGTCTGCTGA
 GTTGCAGTAAGCTATAACCTTGAATCACAA

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FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYPVPRPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLM
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTAEVDLYFDHLSRVVPLQ
YKRGGP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLEPNVQGTQPKMVMMEYWTGWFDWGGPHNILDSSSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAHYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTVVSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPKFNRIYSLDMKKSFFQRFGLDKWXSLEPETPLPAFFLGSL
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGFPLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTTGGCCTTCGGTGGGGGTCAAGACGACGGCACCTACGCCAAAGG
GGAGCAAAAGCCGGGCTCGGCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCGCTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGGTCCC
AAGAAGCTGTCTGCCTTCGTTCCCTGTCTGTGCCGCTCAGCCTGACGCTACTGTGTGCCCA
GGCAGACACTCGGTGTTGTTAGTGGATAGGGGTCTAGACCGGTTTCTCCTAGACGGGGCCC
CGTTCGCTATGTGTCTTGGCAGCCTGCACACTTTCGGGTACCGCGGGTGTCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCTCAACGCCATACAGTTTATGTGCGCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATCTGAGACGAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGCTCTCCCATCCTGGTTGCTTCGAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTTGGCCGAGTGGACTCCTGGTTCAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTTGTCTTTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCCTGTAGATTTTGGGCCAGCTGACAACACTGACCAAAATCTTTACCTGGTT
CGGAAGTATGAACCCCATGGGCCATTGGTAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGCTGTAACCAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTCAACACTTTGGATATTGG
AATGTTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTCTTCGAGATGTCTACAGCAAGT
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCGAGGCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGTTGGGCATTACTGGCTTTCCTAGACTTGTCTTGGCCCCGTGGGGCCAT
TCATTCAACTCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTTGAGGCCAACACCATTTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCTTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCCAATTCCTG
GGGCAACCAATCCTTACCCAGTGGATGATGTTCCCTCGAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCTCCAGTTGCCAAAATGGCCATATCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAAGTCTGGATCAATGGGTTTAACTTGGGC CGGTACTGGACAAAAGCAGGGGCC
ACAACAGACCCCTCTACGTGCCAAGATTCTGTGCTTTTCTAGGGGAGCCCTCAACAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC
CTCAATAGCACTAGTACTTTTGCACAGGACACATATCAATTCCTTTCAAGCTGATACACTGAG
TGCTCTGAACCAATGGAGTTAAGTGGGCAC~~TGA~~AAGGTAGGCCGGGCTGTTGGCTCATGC
CTGTAACTCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGCTGAGGACTCAAGA
CCAGCTTGGCCCAACATGGTGAAACCCGCTCCACTAAAAATACAAAATAGCCGGGCGTG
ATGGTGGGCACTCTAATCCAGCTACTTTGGGAGGCTGAGGGCAGGAGAAATGCTTGAATCC
AGGAGGCAGAGTTGACGTGAGGTGTACCACCTGCACCTCCAGCTGGCTGCACAGTGA
GACACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRHDFLLDGAPFRYVSGSLHYFRVPRVL
WADRLCLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLA GLFRALLGEKILLFTTDDGPEGLKCGSLRGLYTTVD FGPADNM TKIF
TLLRK YEPHG PLVNSEYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM YMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVLGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNM RDKLF LTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGD TFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGCTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATAATGGCCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
CTTTGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTCGGGGGTGCCCGATGCTGCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCAGAAGCTAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACATGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAAAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAGTTAGTCATTACATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAAAGACT
GACTTGTTTAAAAATTATGGCATAACAAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCATTTATTTCTCTAACACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCGAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATCTGTC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACCTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAC
CTTGAGACCGCTGCCAGCCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTTTTGATACCTTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTCTTGCAAAATGGGATTTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTAAAGTAAATGATTAATGACATT
TTCTTACTAAAAAAAAAAAAAAAA

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FIGURE 68

MAYMLKLLISYISIIICVYGFIPLYTLFWLFRIPLKEYSFEKVVREESSFSDIPDVKNDFAPL
LHMVDQYDQLYSKRFGVFLSEVSENKREISLNHEWTFEKLQHHISRNAQDKQELHFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMMIGLESRELRHLKILHVKSNTLVKPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKMMNVAELELQNCLELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESYFSSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSOLTQLELKGNCLELDRLPALGQCRMLKKSGLVVEDHLFDLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCGGACTTTGCATTTCATTCCCTTTTTCATGACAACTGACTTTTTTTATTCTT
 TTTTTCATCTCTGGGCGAGCTTGGATCTTAGGCCGCGCTGGGAAGACATTGTGTTTTACACACATAAGGAT
 CTGTGTTTGGGGTTTCTTCTCCCTCCCTGACATTGGCATGTCTAGTGTGTGTGGGAGGGAGACCAGCTGG
 GCTCAGTGCTTGTCTGCATCTATCTGCTAGGTACATCGAAGTCTTTTGACCTCCATCAGTGATTATGCCTGTC
 ATCGCTGGTGTATCTGGCGGCTTGCTCTGTGCTAGTGTGTGCTGCTGCTTTTACTTTCAAATACACAAC
 CGCTAAAAGCTGCAAGAGAACTTGAAGCTGTGGCTGTAAAAAATCACAACTCCAGACAAGGTGTGGTGGGCCAAG
 AACAGCCAGGCCAAAACCATTTGACACGGAGTCTTGTCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC
 AGTTTTGATTCCCTGCCACCTTGTCTGTGCGACATAAATGAGGCCCTCTGAGTTAGGAAAGGCTCCCTCTCAA
 GCAGAGCCTGAAGACTTCAATGATGTCAATGAGGCCACTGTTTGTGATGTCCAGGCACAGAAGAAGGCACAG
 CTCCCCATCAGTTTTCATGAAAAATACTCAGTGCCTGCTGGGAACCACTGCTGGAGATCCCTACAGAGAGCTTC
 CACTGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGGAACCTCACTGTGGGGGAATGCTGATAAACCACTCA
 CACAGCTGCTATTCTCACACAAATCTACCCCTTGGCTGGCTGGAAGTGTGCTGGAGGTGTCCAGAAA
 GCTGATGTAACACAGAGCCTATAAAAGCTGTGCTCCTTAAGGCTGCCAGCGCTTGGCAAATGGAGCTTGT
 AGAAGGCTCATGCCATTGACCTCTTAATTTCTCTCTGTTTGGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
 AGTGAGAACTGCACCTGGCAATAGAAAGACAGAAAAACAAAGCATCAGAATTATCTTTTCCCTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAAGTGAAACATTAAGTCTTTGACGGAACCTCCAGCAATGGGCCCTGCTAGGG
 CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
 GACTCAGCAAGAATTCAAAGAACTGTCTTTGCTTCTACTACTTTCTCTCTCCTAACATCTCTATTCCAACTGT
 GGGGTTTACCTGGATACCTTGGAGGATCTTCCACGAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
 TGTGTGTGGCACATACAGTTGGAGAAAGATTACAGATAAAACTAAACTTCAAAGAGATTTTCTAGAAATAGAC
 AAACAGTGCAAATTGATTTCTTGGCCATCTATGATGSCCCTCCACCAACTCTGGCTGTATGGACAAAGTCTGT
 GGCGCTGTGACTCCCACTTCCGAATCGTCATCAAATCTCTGACTGTGCTGTGTGTCTACAGATTATGCCAATTCT
 TACCGGGGATTTCTGCTCTCTCACCTCAATTTATGCGAGAAACATCAACATACATCTTTAACTTGTCTTTCT
 GACAGATGAGAGTTATTATAGCAATCTACCTTAGAGGCTTTTAACTCTAATGGGAATAACTTGCACCTAAAA
 GACCCAACTTGCAGACCAAATTTATCAAATGTGTGGAATTTTCTGCTCCCTCTTATAGGATGTGTACAATCAGA
 AAGGTAGAAGATCAGTCAATTACTTTACACCAATATAATCACCTTTCTGCTATCCTCAACTTCTGAAGTGATCACC
 CGTCAGAAACAACTCCAGATTATGTGAGTGTGAATGGGACATAATTTCTACAGTGGAGATATATACATAACA
 TTTGAAAAGACTATACCTTGAATCACCATATTATGTGGATTGAAACCAACTCTTTTGTTCAGTTAGTCTGCAC
 ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCTCTCCCACTCTGACTTTGCACTCTCGAACC
 TACGACCTAATCAAGATGGATGTAGTGCAGATGAACTTCTAAGGTGTATCCCTTATTTGGACATATGGGAGA
 TTCCAGTTTAAATGCCTTTAAATCTTGGAGAGTATGAGCTCTGTATCTGCACTGTAAAGTTTGTATGTGAT
 AGCAGTGACCAACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAAGCAACAGACATTTCTCATATAAATGG
 AAAACAGATTCATCATAGGACCATTCGTCTGAAAGGGATCGAAGTGCAGTGGCACTTTCCTTTCATGTGTTTACGCTCTG
 AATGTGTGATCTAGCGACAATCAGAGTGGGATTTTGTAAATCAACGGGCGAGCTACAAATACCAAGAGCTG
 CAGAACTATTAACTAACAGGTCCAACTTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAATGCTACTCTCGT
 GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACAGGCTGCTGATGAAAAAA

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FIGURE 70

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDDPDGSCSEENIKVFDGTSSNGPLLGGVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDLTLEGSFTSPNYPKHPPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYSIYAENINTSLTCSSDRMRVIIKSYLEAFNSNGNNLQKDPTRCP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGMHNS
VEIIYITEDDDVIQSONALGKYNTSMALFESNSFEKITLESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHE
THA
BETPNQFPNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC
TGCTGCGCGCCGCGCGCTGCGCCTGCCACAGCGCCAGCGGTTTCGACCCCACTGGGAGTCC
CTGGACGCCCGCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTCCGTTGCCAGCTTCGGTAGCGAGTGTTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAAGATAATTACCCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTCAGCAAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTGTGGGGGT
CAGAATATTCCGTGGAACCTGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAGGAA
CTTGAGGTAGCCATTAGGAACAGAAGTACCTGCGTTTGGAGTGTACTATTCCTTTTGA
ATGGTTTCATCCGCTCTTCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACATGCATGACAAATAGACAACTGTCTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTGATGAATATGGGCCCACACTAGATGGCACCATTTCTGTAGTTTGTGAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCAGAAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTCTTAAATGGCCACATCAGGACAGCTGTCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCATGGAGA
AAGCAATGTAACTGGATAAGAAAATTTATTTGGCAGTTCAGCCCTTTCCCTTTTCCCACTA
AATTTTTCTTAAATTACCATGTAAACATTTTAACTCTCCAGTGCATTTGCCATTAAAGTC
TCTTCACATTGATTGTGTTCCATGTGTGACTCAGAGGTGAGAATTTTTTACATTATAGTAG
CAAGGAATTTGGTGGTATTATGGACCGAACTGAAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTAATATGGGGATATTTCTGGGAATGCATTGCTAGTCAAT
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTTATATCGAAACATATGGAACATAGAGAAG
GTACAGTAAAAAATCTGTAATAAATAAGTGTGACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGCTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGGAAGCCTAGGACATT
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAA
GTTTTCTTTCTTCAATTATAAATAACATAAGGTACTGTAACTTTACAAACGTTTAAAT
TTTAAACCTTTTGGCTCTTTGTAATAACACTTAGCTTAAACATAAACTCATTGTGCA
ATGTAA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLEFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVPDVMYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

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AGCAGGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCCTCAACATAGT
TCCAGAGCTCTCCATCCGGCATGTTATTGAGCATGTGCCCTCATATCACCAGTGGCCCAT
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTCCACGCTGGTGTG
CTTCTCATTCCATCTGGACCACGAGGCTCCTGTGTCAAAGGCTCTTTGCGTGCAGAAAGACT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTTGTGAGCAAAAAGGCCAACAGC
AGCTGAATTTTCAGAGAAGCTTAAGGAGGCTGTAGGCTGCTGGGACATAAGTTTGGCCGGCAAG
GACCAAGTTTGAACACGCTTGAAGCTGATCTTTGAACATTCGACGATATGGCTGGGTGGAG
TGGATTCTGTGGTCACTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAAGCCGACAGTATTGCAAGCTATTGTTACAACATCATCTGAT
ACTTGGACATACTCGTGCAATTCAGAAATATTCAACCACAAAGATCCCCATTCCAACATCA
AAGTCGACACAAACACAGAAGATTTATTGTCAGTGACGATACCTACTCGGTGGCATCCCCCT
ACTCTACAATACCTCGCCCTACTACTCTCTCTGCTGCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTGTGTGCACAGAAGTTTATTGGAACATAGCCATGTCTACAGAAGC
TGAACCAATTTGTTGAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGTGTGGAGGTGTCC
CATCGGCTCTGCTAGTGTCTGCTCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTGCT
TATGTCAAAGAGTTATGTAAGGGCTTCCCTTTTACAACAAGAATCAGCAGAGAAGAAATGAT
CGAAACCAAGATGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAGA
AAACTGATATAAACCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGGCATGCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCTCGCCCAAGCTGGGGAATCAAAAGGGCCCAAGAACCAAGAAGAAAGTCCACCTT
GGTTCCTAAGTGAATCAGCTCAGAGCTGCCATTGGCATATGAGGTGCACCAAGAGCAATGC
CCTTCTCCTTATTGTAAACCTGTCTAGATCTCTATCCTCTCACTCAACAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATTCCCCTGGGAGAAAGGAGTTTGCAGAAAGTCAA
GGACATAAAACATCTCATGATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAAGAGTACAGAGACAAGGCTTTCTCTACTGATTCGCGAGCTCAGAC
CCTTCTCTCAGCTCTGAAAGAGAAACGATATCCCACTGACATGCTCTTCTAGCGCCGTA
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCTGGAGATCTCTATAACTTGGAG
ACTTAATCTCTGTAAGAGCTAAAATAAAGAAATGAAGCAAGGCTGAGGATACGACAGTACAT
GTGACAGGGAGCTGAACACAGACAGGCTCAAAGTGTCTTCTGTAACATTAAGTTGGA
ATCATGTTTGAACACACACACTACTTTTCTGGTCTCTACCACTGATCTGATATTTCTCT
AGGAATATACTTTTACAAGTAAACAAAATAAAAACTCTATAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTC
ACAAATCAATTTGCTGAATAGCTACTATGTGTCAGTGTCTGTCAGAGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTTGCATCATAGTAGACGCTATCTGGGAAGCTATTTTTC
GTTTTGATATTTCTAGCTTATCTACTTCCAACATTAATTTTATTTTGTCTGACATCAATCTT
ATTCATTTTCTTAATATGSCAACCATTAACCTTAATTTATATTAACTATCAATGAAG
TACATTTGTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTCCAACAGAAGGGACTGAGAGATGCAGAAATATTTGTGCAAAAAATTA
AGCATTTAGAAAACTT

FIGURE 74

MARCFSLVLLLTISIWTRRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNNEESKKTDKNPPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

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FIGURE 75

AGATGCGGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTACTCTGTGAGGAA
ACTGCCGCGCTCTGCCACGGTCTGCCCACCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGTATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTCGCATGGGCCCTACTTTACATCACACTCTGCATAGTGTTCC
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATGTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAACT
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT
CCAGGCTCTTTCATAACCACAAGCCTGAGGCTGCAGCCTTINATTNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTTAAAGAGGCATCTAGGGAATTGTGAG
GCACCCCTACAGGAAGCCCTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTGAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCTCTTITAG
TTGACCTGCACAGCTTGTTTAGACCTAGATTTAACCCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAAATTTTCCCCAAGGACTCTTGCTTCTTAAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
TCCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLVLRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSPLTQQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

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[illegible]

071031

Signal sequence:

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTGTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGCCAAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCTCTGGGGCGGATCGTGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGAATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACCGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGCGT'TTCCGGGTGGC
CGACCAGGATGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCAACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACACAGCCC
CTGGTGGAAGCCAACCACTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCAGGCATCTCTGCCCCCTGGGCTCTCAGGGACCCCTGGGTGGCTTC
TGTCCTGTGCACCCCCAACCCAGGGAGGGCTGTCTAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

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Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCCTTGCCCTTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
 CGGGCGGGCGCGGGTGGAGGGGATCCCTGACGCTCTGTCCCTGTTTCTTTGTGCGTCCCAG
 CCGTCTGCTGCTCGTTTGGCGCCCCCGCTCCCGCGGTGCGGGGTGACACCGATCCTG
 GGCTTCGCTCGATTTCGCGCCGAGGCGCTCCAGACCTAGAGGGGCGCTGGCTCGGAGCAG
 CGGGTCGTCTGTGCTCTCTCCTCTGCGCGCGCCCGGGGATCCGAAGGGTGGGGGGCTCT
 GAGGAGGTGACGCGCGGGGCTCCCGCACCCCTGGCCTTGCCCGCATTTCTCCCTCTCTCCAG
 GTGTGAGCAGCCTATCAGTCACCAATGTCGCGAGCCTGGATCCCGGCTCTCGGCTCGGTGTG
 TGTCTGCTGCTGCTGCCGGGGCCCCGGGCGAGCGAGGAGCCGCTCCCATTGCTATCACATG
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCCTCGCCACGGGGGTGCC
 CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
 GCTGCTGTCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
 TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
 GGTCTGCTTCTTTCACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCCGAGAAGAAAACTGG
 CAATAAAGATTGTAAGCAGACATTGCATTCTTGATTGATGGAAGCTTTAATATTGGGCAGC
 GCCGATTTAATTACAGAAGAAATTTGTTGGAAGAGTGGCTCTAATGTTGGGAATTGGAACA
 GAAGGACCACATGTGGCCCTTGTTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
 AAACTTTACATCAGCCAAAGATGTTTGTGTTGCCATAAGGAAGTAGGTTTCAGAGGGGGTA
 ATTCGAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCCTCACGGTAGATGCTGGA
 GTAAGAAAAGGGATCCCAAAGTGGTGGTGATTTATTGATGGTTGGCCTTCTGATGACAT
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTATAGTTTCTGTGGCCA
 AGCCTATCCCTGAAGAACTGGGGATGTTTCAAGATGTACATTGTTGACAAGGCTGTCTGT
 CGGAATAATGGCTTCTTCTTACCACATGCCCAACTGGTTTGGCACCAAAAATACGTAAA
 GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATACT
 CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC
 ATGCTTGAATTTGTTTCCAAATAGCCAAAGACTTTTGAATCTCGGACATTGGTGCCAAAGAT
 AGCTGTGTACAGTTTACTTTATGATCAGCGCACGGAGTTCACTTTCACTGACTATAGCACC
 AAGAGAATGTCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
 GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA
 CTTCTAGTAATTGTACAGATGGGCAGTCTCATGATGATGTCCAAGGCCCTGCAGCTGCTG
 CACATGATCGAGGAATCACTACTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTCAACAAGAGAGTTTCAAGGATT
 AGAACCAATTGTTTCTGATGTCTATCAGAGGCATTGTGATAGATTTCTTAGAATCCAGCAAT
AATGGTAAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTTGTATT
 CTCATAACTAGTAAATGCTTTAGCATACTAGAATCAGATACAAAACCTTTAAGTATGTCAAC
 AGCCATTTAGGCAATAAGCACTCCTTTAAAGCGCTGCCTTCTGTTTACAATTTACAGTGT
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
 GATAATGTGGATTAAACCTTAAGAGTCTAACCATGCTCTAATATGTACAGATATGCAAA
 TTCCATAGCTCAATAAAGAATCTGATACTTAGACCAAAAAAAAAA

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FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTTRGLDIRKEKADVLCPPGGCPLEBFSVY
GNIVYASVSSICGAAVHRGVISNSGGFVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFALKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHADAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

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FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCC
GGCGGCCCTCCCGCGGGAGCGAGCAGATCCAGTCCGGGCCGCGAGCGCAACTCGGTCCAGTGC
GGGCGGCGCGCTGCGGGCGCAGAGCGGAGATGAGCAGCGGCTTGGGGCCACCTGCTGTGCCTGC
TGCTGGCGGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGCGCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTGTATGGAGGACACGCGAGCAAAATTGCGCAGCGCGGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACTTACCTCCAGCTAT
CACAAATGAGACCAACACAGACACGAAGTTGAAATAATACCATCCATGTGCAACCGAGAAAT
TCACAAGATAAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAGGAGGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTTGGCAGCTTCCAGTACACCTGCCAGCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGCTGTGGGTCACTGCACCAAAA
TGGCCACCGAGGGGACGAATGGGACCATCTGTGACAAACGAGGGGACTGCCAGCCGGGGCTG
TGCTGTGCCCTCCAGAGAGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCTCCTCTGCCAGCCCCACAGCCACGACCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCGCATGAGTATGAAGTTGGCAGCTTATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCTGACTGAAGAGATGGCGCTGGGGGAGCTGCGGCTGCCGCGCGCT
GCACTGCTGGGAGGGGAAGAGATTAGACTCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCGAGGTGTGTGCTTATAGGCGTGGGCTGACCAGGCTTCTTCTCACA
TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTTCAGC
TCCCCAGGCTGTCTCCAGGCTTACAGTCTGGTGTCTGGGAGAGTACAGGAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTTGATAATTGTTTGGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCTTGCTTTGCAAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTCCACGCAGTCTTTCCATGGGCATAGGTAAGCTG
TGCTTTCAGCTGTGTGCAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTTATTATCC
AGCAGTGTTGCTCAGCTCTTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACGAGAGGCTTTCAT
CTGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACAGCCTTGGTGCCACCA
AAGTGCTCCCCAAAAGGAAGGAGAAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACATAATTTCAATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCGCTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACTTCGAGAAACA
GTACTTAGGTAATTTGATAGGGCAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACTGGAGAAAATCAAAACGAGCAGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTCAGGTGTCA
TGGACTGTGTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTCTTTGAGTTTTAAATATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTTCAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEAAAAKASSEVNLANLPFSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEET

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

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FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACTACCTCACAATCTCTCTGGGCTCAGAAGGACTCTG
 AAGATAACAAATAATTTTCAGGCACTCCACTCTCCTTCCCTGCCAAACACACATGTGGATGTACACACACACATACA
 CACACATACACCTTCTCTCTCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCTATAGAAAGGACAC
 TAAAGCCTTAAGGACAGGCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTGTAGTCAAAAATCACTGGGAGGGG
 CCAGGACCGGTGACTCACACTGTAAATCCGACATTTTGGGAGACCGAGGTGAGCAGGATCACTTGAGGCTCAGGAG
 TTCAGACACAGCTGGCCACTGGAGAAACCCCATCTCTACTAAATAACAAAATTTAGCCAGGAGTGGTGGC
 AGGTGCTCTTAATCCGAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCACT
 CAGCTGAGTGCACCGCTGCACTCCAGCTGGGTGGTGCAGAAATGAGACTCTGTCTCAACAAACAAACACGGGAGGA
 GGGGTAGATGACTGCTTCTGTCAACCTCTTAACTCGCATCCTCTTCTTCCAGGCTGCCCTGTATGGGAGCTG
 GCAATGACTGAGCAGGCGCCAGCCCAAGGACAAGGAGAAAGGCAATTTGAGGAGGGGCAAGAAAGTGACGCCCG
 GTGTAGATGACTGCCCTGGGAGGTTGGTCTTGGGCCCTGGCAGGGTGTCTGACCCCTTCCAGTCTGCAAAACACA
 AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTCTCTGTGGCCCC
 ACTCTTGTGACTGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCGTGGTACCTGGCATGTTCCCTGCCCCCTCA
 GTGTGCTGCCAGATCCGCGCCTGGTATACGCCCCGCTGCTCTACCGGAGGCTACCACTGTGGACTGCAATGA
 CCTATTCTGACCGGAGTCCCCCGGCACTCCCGCAGGCAACAGACCCCTGCTCTGTCAGAGCAACAGCATTGT
 CGGTGTGGACAGAGTGAAGTGGGCTACCTGGCCAACTCTACAGAGCTGGACCTGTCCCAAGAACAGCTTTTCGGA
 TGCCCGAGACTGTGATTTCCATGCCCTGCCAGCTCTGAGCCTGAGAGGAGAACCAGCTGACCCGGCT
 GGAGGACCAAGACTTTGCGAGGCTGGCCAGCTTACAGGAACCTATCTCAACCAACAGCAGCTTACCGCACTGC
 CCCAGGCGCTTTTCTGGCTCTCAGCAACTGTCTGGGCTGCACCTCAACTCCAGCTCTGTGAGGCGCACTGAC
 CCGCTGGTTTGAATGCTGCCCACTTGGAGATCTCATGATTGGCGGCAACAGGTAGATGCCATCTGGACAT
 GAATCTCCGGCCCTTGGCCAACTGCGTAGCCTGGTGTCTAGCAGGCAATGAACCTGGCGGAGATCTCCGACTATGC
 CCTGGAGGGCTGCAAGGCTGGAGAGCTCTCTTCTATGACAACAGCTGGCCCGGGTGCACAGGCGGGCACT
 GGAACAGGTGCCCGGCTCAAGTCTTAGACCTCAACAGAACCCGCTCCAGCGGGTAGGGCGGGGGAATTTG
 CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAAATGAGGAGCTGGTCTCATGACAAGTTTGGCCTGGT
 GAACCTCCCCGAGCTGACCAAGCTGGACATCAACAAATACCCAGGCTGTCTTCTATCCACCCCGCGCTTCCA
 CCAGCTGCCAGATGGAGGACCTCATGCTCAACAAACAGCTCTCAGTGGCTTGCACAGCAGAGCGGTGGAGTC
 CTTGCCCAACTCTCAGGAGGTAGGTCTCCAGGCAACCCCATCCGCTGTGACTGTCTATCCGCTGGGCCAATGC
 CACGGGCAAGCTGTGCTGTCTCATGAGCGCAATCAACCTGTGTGGGAGCTCCCGAACCTCCAGCCCTCC
 GGTCTCAGCTGGCTCTTCCGAGGATGACGGACCACTGTTTGGCCCTCACTCCCAAGAGCTTCCCCCAAG
 CCTCAGGTAGCCAGTGGAGGAGCATGGTGTGCTGCAATGCCGGGCTGAGCCGGAACCCGAGATCTACTG
 GGTCACTCAGCTGGGCTTGCATGTACACTGCCATGCCATGAGGAGGAGTACCGGGTGTACCCCGAGGGGAGCCT
 GSAGCTGGCGAGGCTGAGCAGAGAGAGGCGAGGCTATACACTGTGTGGCCCAAGAACCTGGTGGGGCTGACAC
 TAAGACCTGTAGTGTGCTTGGCGCTGTCTCTCTCCAGCAGGAGGAGTACCGGGTGTACCCCGAGGGGAGCCT
 GTGGCAGGAGACCCACCCCTATACATCTCTGCTATCTTGGCTCACCCCAACCAACAGTGTCCACACACTCAC
 CTGGTCCAGTGGCTCTCTCTCCGCGGCGAGGAGGCACTGCTGGCCGGCTGCTGCAAGTGGCTTGTGCTATGCCACACCA
 CAACATATCCCGCTCTCTTCCAGGCGAGGAGTACTGGGCTGGCTGCAAGTGGCTTGTGCTATGCCACACCA
 GTTGGCTTGTGTATGGGCGAGGACAAAGAGGCGCACTTCTTGGCCACAGAGCTTAGGGATCGCTCTGGCTGCT
 TGGCATCTGGCTCTGCTGTCTCTTCTCTGGCAGCTGGGCTAGCGGCCACTTGGCAGAGGCAACCCAGGAA
 GGGTGTGGGTGGGAGGCGGCTCTCTCTCAGCCTGGCTTCTGGGGCTGGAGTGGCCCTTCTGTCCGGTGT
 GTCTGCTCCCTCTGCTCTGCCCTGGAATCCAGGAGGAAAGCTGCCAGATCTCAGAAAGGAGACACTGTGGC
 ACCATTGTCTCAAAATCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAA
 AGAAGACAGCTTGGGCGAGATGCCCTGCCAGGAAAGGACATGGAACCAAGTGGTTGAGGCTGGCAGCTGGG
 CAGAGCAGATGGGGCTTTTGGCCCTGGGGGTGCTTCTGCAGCTTGAAGAAAGTGGCCCTTACCTCTATAGGCTA
 CTTCTGCTGCATCTTGAAGACATCTCCAGGAAACAGGAGGACTTGGTGCAGAGCTCTGGCTGCCACTCTT
 CTCTTCCCGAGAGGCTCTTGGGCTGGCTTGGCTGCTCCCTACCTGTGTGCCCGGGCTGACACCCCTTCTCTT
 TCTTTCTCTGTACAGCTCAGTTGCTTGTCTTGTGCTCTGGGCAAGGGCTGAAGAGGCGCATCTCATCTCAG
 CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGGAGATGCCAGGAA
 GCTCATCTCAGAGCTGGGCTGGCATTCGAAAGCTGACTTCTATAGGCAATTTGTAGTCTTTGTGGAGAA
 ATGTGTCACTCCCAACCCGATCTACTCTTTCTCTGTTTGTAAATAATAAAATAAATAATAAATAA
 AAAA

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FIGURE 86

MRLLVAPLLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLQLQSNISIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLFNLEILMIGGNKVDAIILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSLESLSFYDNO
LARVPRRALQVPGCLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPL
ELTKLDITNNPRLSFIHPRAFHHLPMETMLMNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLLTPAHAGRRYRVYPEGTLLELRRTABEAGLYT
CVAQNVLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPHYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRV
SAPLVLPWNPRKLPSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

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FIGURE 87

GCACGGCAAGGCGCTGTTTGAAGAAGTTCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGCGGCGAGACCATCATCAAGGTGATCAAGTTTCATCTCATCATCTGCTACACCGTCTACTAGCTGCACAA
CATCAAGTTTCGACGTGGAGCTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGACCTTACCGCTGTGGCCACCC
CCTGGCCACATCTTCAAGATCTTGGCGTCTCTTACATCAGCCTTAGTCATCTTCTACGGCCCTCATCTGATGTGA
CACTGTGTGGTGTGCTACCGCGCTCCCTCAAGAAGTACTGTTTGTGATCGATCCGCTGAGGAGAGCAGCTACAG
CGACATCCCCGACGCTCAAGAACGACTTCGCGCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCGCTCTTCTCGTGGAGGTGAGTGAGAACAGCTGCGGAGCTGAACTCAACAACGAGTGGAGCGCT
GGACAAGCTTCGCGGACGCGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCACTGCTCAGTGGCAT
CCCTGACATCTGTTTGACTCCGCTGGAGCTGGAGTCTCAAGCTGGAGCTGATCCGCGAGCTGACCATCCGCGC
CAGCATCTGCCAGCTCAGCGGCTCAAGGAGCTGTGGCTCTACACACAGCGGCGAAGATTGAAGCGCCTGGCGCT
GGCCTCTCTGCGGAGAGAACTCGCGGCGCTGCACATCAAGTTCAACGACATCAAGAGAGATCCGAGCTGTGGATCTA
TAGCTGGAAGACCTGGAGGAGCTGCACCTGCAGCGGCAACCTGAGCGGAGAGAACACCGCTACATCGTCATCGA
CGGCTGCGGAGCTCAACGCGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCTGCACCTGCAGAACTGTCCATCAACAATGAGGGCACCAGCTCATCTGCTTCAACAGCCTCAA
GAAGATGGCGAACTGACTGAGCTGGAGCTGATCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAAACCTCAAGACCATCGAGGAGATCATCAGTCTCCAGCACCT
CTGCGCAGCTCAGCTGCTTAAGCTGTGGTCAACCAACATCGCTACATCCCATCCAGATCGGCAACCTCACCCT
CCTGGAGCGCCTCTACCTGAACCGCAACAGATCGAGAAATCCCCACCCAGCTCTTCTACTGCGCGAAGCTGGCG
CTACCTTGAACCTCAGCCCAACCACTGACCTTCTCTCCCTGCGACATCGGCTCTGCGAGAACCTCCAGAACCT
AGCCCTCAGCCGCAAGCAGTGCAGGAGCGCTCTCCCTCGGAGCTCTTCAGGACCCGCTTCTGCGAGCTCGGCGCCTGCACCT
GGGCAACACAGCTGCTCAAGCTCACTGCCCTCAGGGGTGGCGAGCTGCACCATGACAGCAGTGCAGTGCAGTGGGG
CAACCGGCTGAGTGCCTGCCTGTGGAGCTGGCGGAGTGCCCACTGCTCAAGCGCAGCGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGCTGACAAAGCGCAGCGCTGAGCGAG
GCGCGCCAGCACAGCAGCAGGAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGAGGCCCTAGCTTCTCCAG
AATCCCCGACAGCCAGGACAGCTCGCGGCTGGCGAGGAGCTGGGCGCGCTTGTGAGTCAAGGCCAGAGCGAG
GGACAGTCTGTGGGGCTTGGCCCTTTTCTCCCTCTGAGACTCAGCTCCCGAGGAGAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCTCTCGGGAGGACAGCTCTGCCCGAGGGGCTGAG
CTGCCACAGAGGCTCTGGGACCTCCTTCTTAGTTCTTGGTATTATTTTCTCTCATCTCCCACTCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTCAAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGGCTGCTCTTTCCCC
TTGTCTTATTTAGCGATGCGCGCGGCATTAAACCCACCTGGAATTCAGCAGAGTGGTCCGGGGCGAACAG
CCATGGGACGCTACCCAGCAGTGCAGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCGTGGAGCTTGCCTCTTCAAGTTTGTGGCAGTTTGAATTTTGTGTTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTTAAAAAAGCTTTGAAAAATGGATGGTTTGGGTATTAAGGAGAAAAAATTTAAAAA
AAAAAGACATAACGGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAGCAGCCAGACGT
TGAATGTGTTTCTTCTCTGGGCGCAGGGTGCAGGGTGCTTCCGGATCTGCTGATCTTGGTCCAGGAGTT
CTATTTGTCTTGGGGAGGAGGTTTTTTTTTGTGTTTTTGGGTTTTTTTGTGCTGTTGTTTCTTCTCTCC
ATGTGCTTGGCAGGCACTATTCTGTGGCTGTGCGGCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGAGGAG
ACTCGGGTTGGCTAATCCCGGATGAACGGTGTCTCATTGCGACCTCCCTCTCGTGCCTGCTGCTTCTCTCA
CGCACAGTGTTAAGGAGCCAAGAGGAGGCCATTCGCGCAGACTTGTGTTCCCACTCTCTGCGCATGGGTGTGT
CCAGTGCCACCGCTGGCTCCGCTGCTTCCATCAGCCCTGTGCGCACTGGTCTTCAATGAAGAGCAGACATTA
GAGGCTGTGCGGGAATGGGAGGTCGCCCCGGGAGGCGAGGCGTGTGTTTCAAGCGCGTTCCGCTCTTGGCGC
CTGGAGTGCACAGCCAGTCCGCACTGGTGGCTGGAAGCAACCTGCTTTAGATCACTCGGCTCCCACTCT
AGAAGGCTCCCGCTTAGATCAATCAGGTGACACTAAGGCACGTTTAGAGATCTCTGTGCTTAATGATTATGT
CAATCGCTGCTGCTGCTTGTGTTTTCTGCGTGTCAATGGATATAATCTCAGAAATAATGCACATAG
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGTGAACTGTAGACTCGGTACAGATATCAATAAA
ATCTATAACAGAAAAA

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FIGURE 88

MRQTIKVIKFIILICYTVYYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDDKLRQRLTKNAQDKLELHLFMLSIGIPDVTVDLVELEV
LKLELIPDVTIPPSTIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLYDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTGTCTGCTGCTGCCGCTGCTGCTGGGCTGAACGCAGGAGCTGTCATTGACT
GGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTTGCTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTCTAGCACTGGATTGGAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACACGGAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCACCTGGGTTCAGTTATGTGAATGGTAGTGGTGCCATATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTCTGGATCTCCCTGTTGATTCCGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGSTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGGCCACCTAGTTTGTCTTTGTACGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG
GGTGCGGAAACTGAAGTGGCCAGAACTGCCATAATTTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCCATAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTT
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAATATTCTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTTTGATCAAAATAAAGGATGATAATAGATATTAA

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FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPFVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELWGKAEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKFPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYS DPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

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FIGURE 91

GGCCGCGGGAGAGGAGGCC**ATG**GGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCAGCGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACTTACCTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCGCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGA**GC**CTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTGTTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGPCRRVITSRIVGGEDAE LGRWPWQGSRLW
DSHVCVGSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSN I
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

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FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGCCCTCATCTCTCTGGCAAAATGCAGTTACAGCCCGGAGCCCGACAGCGGAGGACGC
 TGCCCCCAGGGCTGGGTGTCCCTGGGCCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTTT
 GCCCTGAGACAGCAGAAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGATCCACAG
 CTCTCCTCAATACGGAATAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
 CACTGACCTCCACACGGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCCAGAAAGTGGCAATTCT
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC
 ATCCCTACCAGCTTCCACAGGCCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
 TTTCCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCGCT
 GCATCTGGGGGTAACCCCTCTGTGATCCGTAAGCGATACAACTTGACCTCACAAGACGTGG
 GCTCTGGCACCAAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGCACT
 ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
 ACAGTGAAGCTCATGAAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCTCAGGTGACAGT
 GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACCAGTTCGCCCTACCTTCCTGCGCTCCAG
 CCCCTATGTACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCAAAATGAAA
 TTGTTGACTATATCAGTGGTGGTGGCTTTCAGCAATGTGTTCCACCGGCCTTCATACCAGGAG
 GAAGCTGTAAACGAAGTTCCTGAGCTTAGCCCCACCTGCGCACCTCCAGTTACTTCAATGC
 CAGTGGCCGTGCCATACCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTCTACTCCAGTGGTTTGGGGGGATCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTTGGCTTTCTCAACCCAAG
 GCTCTACCAGCAGCATGGGCGAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTCTGTC
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTCGGCTGGGATCCTGTAAACAGGC
 TGGGGAACACCAACTTCCAGCTTTGCTTGAAGACTCTACTCAACCCCTGACCCTTTCCTATC
 AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTTCACTCCCTTATTCTGCCCTGTTG
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGTGAAA
 TGCTGTGAGCTTGACTGACTCCCAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
 CCTGCTTGAATTCCTCAATAAGATGCTGTAAGTACATTTTGAATGCGCTCTCCCTCGCG
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCAAAGGGTTGTATACAGACTCTGTGCACTA
 TTTCACTTGATATTCATTCCTCAATTCAGTGCAAGGAGACCTTACTGTACCGTTTACTCT
 TTTCTACCTGACATCAGAAACAATGGCCTCCAGTGCATACTTCAATCTTTGCTTTTATG
 GCCTTTCCATCATAGTTGCCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTGT
 ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
 TCCATTTGTAGATTTTGTCTCTTCTGACTTTACTCATTTGCTCCCTGGAACAAATCACTGACA
 TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAAATATGATGTATACCTCAA
 TGTAaaaaa

FIGURE 94

MGLQACLLGLFALILSGKCSYSEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWL LAAGA QKCHSVITQDFLTCWL
SIRQAELLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGG LHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDESLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPSSSYFNASGRAYPDVAALSDGYWVVSNRVIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPWPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCTCCTGTGCTCTTGCCCCAGTCTACCCCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCCAAGTGTCTATAAGGGAAC
CCACTGCCCACCTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGTCCTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTTCAGCATTTTGGGAAGGACTTCCTGCTCAACTACCTTTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCTGGTGGCAGAGAAGCATGTCTTCACAGCTGCCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGGTGGTTCGAGGGGCCAACGACTCCAGCTTCAGCCATGCCCGAGCAGATGAA
ATTTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTTCAGG
GCACCAAGTGGGTGGACATGAATGGTTCCTCCACAGGATTTCAACGTGGCTGTCTAGAATCACTC
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGGAGGGG
TGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTCTTATTTTAGGAGAGGCC
AAATTGTTTTTTGTTCATGGCGTGACACGTGTGTGTGTGTGTGTGTGTGTGAAGGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG
GTTTGTGTATCATATCATATATCATTAAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA
AAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTGATTTTATTTTCATCTGAACCTGTTTCAAAGATTATATTAATAATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

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FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD SGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDA
LLELKKPKHRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQKWERKIIGIFSGHQWDMNGSPQDFNAVAVRITPLKYAICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

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FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGTTGGTGT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGTGGGTGTTGCTGGGTGGAGC
CCCACCTGTGTATTCTTGAAGGAAGGTGCCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCCTCTATCCACCT
CCCTCCAAACACCCACTGTCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC
CCCACCTCAGACCCTGCAGAAGCTGAAGGTTCTTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGTACTT
GGAGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCTCATGTGCCAGGTGGAGC
GCGCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC
GGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGGCGGCTCGGGCGGTTTCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCGACCCGCCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTGTAAACCCTGCCACATATCTTATTATTCTCCAATTCAATAAATTATTATT
CTCCAAAAA

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><subunit 1 of 1, 317 aa, 1 stop

MVVS GAPPALGGGCLGTFSTLLLLASTAI LNAARIPVPPACGKPPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLTTSRWVITA AHCFKDNLNKPYLFSVLLGAWQLGNPGRSRQKVGVA
WVEPHFPVYSWKEGACADIALVRLERSIQFSEVLPICLPDASIHLPNTHCWSIGWSIQDG
VPLPHPQTLQKLKVPIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWEGCAERNRPVGYISLSAHSRWSWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

amino acids 1-32

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

amino acids 826-830

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

amino acids 607-615

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
AACAAGGAGCGCGGGCGCGCGCGGAGAATCTGTTGCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCGAGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCTCACTTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCGTTACCTGGTAACTGAGGCCCCATCCTTCGGGGGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCTTGCAACCAAGGCTCTGCCTGTGTGGAAACCCAGGCC
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCATGTTCCTATCCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAAGGCTGAACCTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCTGTGTCATCTTCCCCACCTGTGCCGACCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCTCGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCGCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT
GATGCTTACCTGGCTGGGGTGTCTGCCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCTTAGGGGCAGATGAAGGACAAAGCCCACTGAGTGGGGTTC
TTTGTAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

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FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPGVGTDEEKRLMVELHNLRYAQVSPITASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGQVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAATEASDRKMGTPSSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAC TGAAGT CAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCCGGTCATTCTCCAAGTATGGTGGACGT
 ACTTCTGTGTCTCCCTCTGCTTGCTTTTTCACATTAGCAGACCGGACTTAAGTCAACAACAGATTATCTTTTCAT
 CAAGGCAAGTTCCATGAGCCAGCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCC
 AAATCTGGGACAGCTCTCGGCAAAATATTACACTTCTCTCCTTGCGTGGAACAGGATTTGTTGAAATACCTCCCTGA
 ACATCTGAAGAAGTTTCAGTCCCTTGTAAGCTGGAACGGAACCAATATTTCAGAGCTCCAAACTGCATT
 TCCAGCCCTACAGCTCAAAATATTCTGATATCTCAACAGCAACCGAGTCACATCAATGGAACTCCGGTATTTTGACAA
 TTTGGCCCAACA CACTCTCTGTGTTAAAGCTGAACGGAACCGAATCTCAGCTATCCCAACCAGAGATGTTTAAACT
 GCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGAATGACATTCCAAGGCCCTTGG
 TGCTCTGAAGTCTCTGAAATGCAAGAAGTTGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA
 CATGGAAATTTTTCAGCTGGACCAATAACCACTTAACAGAGATTACCAAAAGGCTGGCTTTACGGGCTTGCTGATGCT
 GATCTGAAGTCTCTGAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTCGGAGTCTTGCCAGAAGTCTCAG
 TGAGCTGGACCTAATCTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGCCCTAAGCTTACTAAATAC
 ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGGCTTTCAGTTTAAAGACTTT
 GGATCTGAAGAACAATGAAATTTCTCTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAACTGAG
 GCGACTGTATCTCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCCTTCACTGGTTTGGATGCATTTGGAGCA
 TCTAGACCTGAGTGAACAACCAATCATGTCTTTACAAGGCAATGCATTTTACAATAAGAAACCTGCAACAATT
 GCATTTAAATACATCAAGCCTTTTGTGCGATTGCGAGTTGCGAGTCCCACTGAGTGGGTGGCGGAAAAACAATT
 CTAGAGCTTTGTAATAGCCGATTTGCGCCATCTCAGCTGCTAAAGGAAGAAGCAATTTTGCTGTAGCCCAATGA
 TGGCTTTGTGTGTGATGATTTTCCCAACCCAGATCAGGTTTCAGCAGCAACAGCTGCGCAATTAAGGATTC
 CAAITTTGAGTTTCACTTGCTCAGCTGCGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTGGAAAAAGACATGA
 ACTACTGCTAGTCTGAAATGGAATTTATGCACACTCCGGGCCAAGGTTGGCGAGGTGATGGAGTATACCAAC
 CATCTCTCGGCTGCGCGAGGTGGAATTTGCGAGTGAGGGGAAATATCAGTGTGTCACTTCCCAATCACTTTGGTTC
 ATCTACTCTGTCAAAGCCAGCTTACAGTAAATATGCTTCCCTCAITTCACCAAGACCCCACTGATCTCACCAT
 CCGAGCTGGGGCCATGGCAGCCTTGGAGTGTGCTGTGTGGGCAACCCGCCCCCAGATAGCCTGGCAGAAGGA
 TGGGGGCGAGACTTCCAGCTGCAAGGAGAGACGCAATGATGTGATGCCCGAGGATGACGTGTTCTTTATCGT
 TGGGTGAAGATGAGGACATTTGGGGTATACAGCTGCACAGCTCAGAACAGTCAAGGAAGATTTCAGCAAAATGC
 AACTCTGACTGTCTAGAAACACCATCAATTTTGGGCCACTGTGGACCGAACTGTAAACCAGGGAAGAACAGC
 CGTCTTACAGTGCATTCTGGAGGAAGCCCTCCCTCAAAGTGAACCTGAGCTGAGCAAAAGATGATAGGCCCATTTGTGT
 AACCAGAGGCACTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGAGTGTGCTGGGAA
 ATACACATGTGAGATGCTTAACACCCCTTGGCACTGAGAGAGGAACGTCGCGCTCAGATGTGATCCCACTCCAAC
 CTGGCACTCCCTCAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAGC
 CGTGGTTTGTGTGTGGGCAAGTCACTCGTGTGGGTGCTCATATATACCAACAAGGCGGAGGAATGAAGA
 TTGCAGCATTACCAACAAGATGAGCAACTTGGCAGCAGATATTCCTAGTTATTGTGATCTCAGGGAACGTT
 AGCTGACAGGCGAGATGGGTACGTGCTTTCAGAAAGTGAAGGCCACCAGCTTTGTGCATCTTCAGGTGCTGG
 ATTTTCTTACCAACAACATGACAGTGTGGGAGCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAGCTGC
 CACAGATCTGTTCTTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTGAAGGGAATGTGATGGCTCAGA
 TCTTTTGAACATATCATACAGGTTGTCAGTCTGACCAAGAACAGTTTAAATGGACCACTATGAGCCCAAGTGA
 CATAAAGAAAAGGAGTGTACCCATGTTCTCATCTTCAGAAGAACTCTGCGAACGGAGCTTCAGTAATATATC
 GTGGCCTTCAGATGTGAGGAAGCTACTTAAACATAGTTACTCTCACAATGAAGGACCTTGAATGAAAAATCTGTG
 TCTAAACAAGTCTCTTTAGATTATTAGTGCAAAATCCAGAGCCAGCGTTCGGTTGCTCGAGTAATCTTTCATGGG
 TACCTTTGGAAGAGCTCTCAGGAGACCTCACTTAGATGCCATTCAAGCTTTGGACAGCCATCAGATTGTGACGG
 AAGACCTTTTATTGAAAGCTCACTTCTCCCAAGTTTGACTTGGAGTCAGAGGAGATGGGAAGAAAGAGAC
 AGATTTCAGGAAGAAAATCAATTTGTACCTTTAAACAGACTTGAAGAACTACAGGACTCCAAATTTTCAGTC
 TATAGCTTTGGACACATAGACTGAATGAGACAAAGGAAAGCTTAACACTACTCAAGTGAACCTTTTAAACTTA
 AAAGGAGAGAAATCTTATGTTTTTAAATGGAGTATGAATTTAAAGGATAAAAATGCTTTATTTATACAGAT
 GAGCAAAATTAACAAAGTTATGAAAGTTTATTAAGTGGAAATGATGCTCATATAAGATACCTTTTAAACTTA
 TTTTAACTTTGTTTTTGTCAAAAAGATATCTTACGTAAATTAATGATATAATCATGATTTATTTATGATTT
 TATATAGGCCAATCTTTTATGGAAGAAATGAGTTACTAAAGACTTTTAAATCAACTCTGCTTGTACCAATTT
 TTAATAGAAGTTACTTCAATATATTTTGCACATATATTTAATAAAATGTGTCAATTTGAA

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Figure 1. The effect of the concentration of the *Agaricus bisporus* spores on the growth of *Agaricus bisporus* on the substrate. The concentration of the spores was 10⁴ spores/g (a), 10⁵ spores/g (b), 10⁶ spores/g (c), 10⁷ spores/g (d), 10⁸ spores/g (e), 10⁹ spores/g (f), 10¹⁰ spores/g (g), 10¹¹ spores/g (h), 10¹² spores/g (i), 10¹³ spores/g (j), 10¹⁴ spores/g (k), 10¹⁵ spores/g (l), 10¹⁶ spores/g (m), 10¹⁷ spores/g (n), 10¹⁸ spores/g (o), 10¹⁹ spores/g (p), 10²⁰ spores/g (q), 10²¹ spores/g (r), 10²² spores/g (s), 10²³ spores/g (t), 10²⁴ spores/g (u), 10²⁵ spores/g (v), 10²⁶ spores/g (w), 10²⁷ spores/g (x), 10²⁸ spores/g (y), 10²⁹ spores/g (z), 10³⁰ spores/g (aa), 10³¹ spores/g (ab), 10³² spores/g (ac), 10³³ spores/g (ad), 10³⁴ spores/g (ae), 10³⁵ spores/g (af), 10³⁶ spores/g (ag), 10³⁷ spores/g (ah), 10³⁸ spores/g (ai), 10³⁹ spores/g (aj), 10⁴⁰ spores/g (ak), 10⁴¹ spores/g (al), 10⁴² spores/g (am), 10⁴³ spores/g (an), 10⁴⁴ spores/g (ao), 10⁴⁵ spores/g (ap), 10⁴⁶ spores/g (aq), 10⁴⁷ spores/g (ar), 10⁴⁸ spores/g (as), 10⁴⁹ spores/g (at), 10⁵⁰ spores/g (au), 10⁵¹ spores/g (av), 10⁵² spores/g (aw), 10⁵³ spores/g (ax), 10⁵⁴ spores/g (ay), 10⁵⁵ spores/g (az), 10⁵⁶ spores/g (ba), 10⁵⁷ spores/g (bb), 10⁵⁸ spores/g (bc), 10⁵⁹ spores/g (bd), 10⁶⁰ spores/g (be), 10⁶¹ spores/g (bf), 10⁶² spores/g (bg), 10⁶³ spores/g (bh), 10⁶⁴ spores/g (bi), 10⁶⁵ spores/g (bj), 10⁶⁶ spores/g (bk), 10⁶⁷ spores/g (bl), 10⁶⁸ spores/g (bm), 10⁶⁹ spores/g (bn), 10⁷⁰ spores/g (bo), 10⁷¹ spores/g (bp), 10⁷² spores/g (bq), 10⁷³ spores/g (br), 10⁷⁴ spores/g (bs), 10⁷⁵ spores/g (bt), 10⁷⁶ spores/g (bu), 10⁷⁷ spores/g (bv), 10⁷⁸ spores/g (bw), 10⁷⁹ spores/g (bx), 10⁸⁰ spores/g (by), 10⁸¹ spores/g (bz), 10⁸² spores/g (ca), 10⁸³ spores/g (cb), 10⁸⁴ spores/g (cc), 10⁸⁵ spores/g (cd), 10⁸⁶ spores/g (ce), 10⁸⁷ spores/g (cf), 10⁸⁸ spores/g (cg), 10⁸⁹ spores/g (ch), 10⁹⁰ spores/g (ci), 10⁹¹ spores/g (cj), 10⁹² spores/g (ck), 10⁹³ spores/g (cl), 10⁹⁴ spores/g (cm), 10⁹⁵ spores/g (cn), 10⁹⁶ spores/g (co), 10⁹⁷ spores/g (cp), 10⁹⁸ spores/g (cq), 10⁹⁹ spores/g (cr), 10¹⁰⁰ spores/g (cs), 10¹⁰¹ spores/g (ct), 10¹⁰² spores/g (cu), 10¹⁰³ spores/g (cv), 10¹⁰⁴ spores/g (cw), 10¹⁰⁵ spores/g (cx), 10¹⁰⁶ spores/g (cy), 10¹⁰⁷ spores/g (cz), 10¹⁰⁸ spores/g (da), 10¹⁰⁹ spores/g (db), 10¹¹⁰ spores/g (dc), 10¹¹¹ spores/g (dd), 10¹¹² spores/g (de), 10¹¹³ spores/g (df), 10¹¹⁴ spores/g (dg), 10¹¹⁵ spores/g (dh), 10¹¹⁶ spores/g (di), 10¹¹⁷ spores/g (dj), 10¹¹⁸ spores/g (dk), 10¹¹⁹ spores/g (dl), 10¹²⁰ spores/g (dm), 10¹²¹ spores/g (dn), 10¹²² spores/g (do), 10¹²³ spores/g (dp), 10¹²⁴ spores/g (dq), 10¹²⁵ spores/g (dr), 10¹²⁶ spores/g (ds), 10¹²⁷ spores/g (dt), 10¹²⁸ spores/g (du), 10¹²⁹ spores/g (dv), 10¹³⁰ spores/g (dw), 10¹³¹ spores/g (dx), 10¹³² spores/g (dy), 10¹³³ spores/g (dz), 10¹³⁴ spores/g (ea), 10¹³⁵ spores/g (eb), 10¹³⁶ spores/g (ec), 10¹³⁷ spores/g (ed), 10¹³⁸ spores/g (ee), 10¹³⁹ spores/g (ef), 10¹⁴⁰ spores/g (eg), 10¹⁴¹ spores/g (eh), 10¹⁴² spores/g (ei), 10¹⁴³ spores/g (ej), 10¹⁴⁴ spores/g (ek), 10¹⁴⁵ spores/g (el), 10¹⁴⁶ spores/g (em), 10¹⁴⁷ spores/g (en), 10¹⁴⁸ spores/g (eo), 10¹⁴⁹ spores/g (ep), 10¹⁵⁰ spores/g (eq), 10¹⁵¹ spores/g (er), 10¹⁵² spores/g (es), 10¹⁵³ spores/g (et), 10¹⁵⁴ spores/g (eu), 10¹⁵⁵ spores/g (ev), 10¹⁵⁶ spores/g (ew), 10¹⁵⁷ spores/g (ex), 10¹⁵⁸ spores/g (ey), 10¹⁵⁹ spores/g (ez), 10¹⁶⁰ spores/g (fa), 10¹⁶¹ spores/g (fb), 10¹⁶² spores/g (fc), 10¹⁶³ spores/g (fd), 10¹⁶⁴ spores/g (fe), 10¹⁶⁵ spores/g (ff), 10¹⁶⁶ spores/g (fg), 10¹⁶⁷ spores/g (fh), 10¹⁶⁸ spores/g (fi), 10¹⁶⁹ spores/g (fj), 10¹⁷⁰ spores/g (fk), 10¹⁷¹ spores/g (fl), 10¹⁷² spores/g (fm), 10¹⁷³ spores/g (fn), 10¹⁷⁴ spores/g (fo), 10¹⁷⁵ spores/g (fp), 10¹⁷⁶ spores/g (fq), 10¹⁷⁷ spores/g (fr), 10¹⁷⁸ spores/g (fs), 10¹⁷⁹ spores/g (ft), 10¹⁸⁰ spores/g (fu), 10¹⁸¹ spores/g (fv), 10¹⁸² spores/g (fw), 10¹⁸³ spores/g (fx), 10¹⁸⁴ spores/g (fy), 10¹⁸⁵ spores/g (fz), 10¹⁸⁶ spores/g (ga), 10¹⁸⁷ spores/g (gb), 10¹⁸⁸ spores/g (gc), 10¹⁸⁹ spores/g (gd), 10¹⁹⁰ spores/g (ge), 10¹⁹¹ spores/g (gf), 10¹⁹² spores/g (gg), 10¹⁹³ spores/g (gh), 10¹⁹⁴ spores/g (gi), 10¹⁹⁵ spores/g (gj), 10¹⁹⁶ spores/g (gk), 10¹⁹⁷ spores/g (gl), 10¹⁹⁸ spores/g (gm), 10¹⁹⁹ spores/g (gn), 10²⁰⁰ spores/g (go), 10²⁰¹ spores/g (gp), 10²⁰² spores/g (gq), 10²⁰³ spores/g (gr), 10²⁰⁴ spores/g (gs), 10²⁰⁵ spores/g (gt), 10²⁰⁶ spores/g (gu), 10²⁰⁷ spores/g (gv), 10²⁰⁸ spores/g (gw), 10²⁰⁹ spores/g (gx), 10²¹⁰ spores/g (gy), 10²¹¹ spores/g (gz), 10²¹² spores/g (ha), 10²¹³ spores/g (hb), 10²¹⁴ spores/g (hc), 10²¹⁵ spores/g (hd), 10²¹⁶ spores/g (he), 10²¹⁷ spores/g (hf), 10²¹⁸ spores/g (hg), 10²¹⁹ spores/g (hh), 10²²⁰ spores/g (hi), 10²²¹ spores/g (hj), 10²²² spores/g (hk), 10²²³ spores/g (hl), 10²²⁴ spores/g (hm), 10²²⁵ spores/g (hn), 10²²⁶ spores/g (ho), 10²²⁷ spores/g (hp), 10²²⁸ spores/g (hq), 10²²⁹ spores/g (hr), 10²³⁰ spores/g (hs), 10²³¹ spores/g (ht), 10²³² spores/g (hu), 10²³³ spores/g (hv

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGGTGCCTTGCAAAAATG
 AAGGATTCGACGACGAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTCGAAGAGAAAGGAAC
 GAAGCTTTTTCTTGAGCGCTTGGATCTTAACACAAATGGTATATGTGTCACAGGGAGCATTCAGAATGA
 TAAACAGAGTTAGACCCGCGGGGTGGTGTGTCTGACATAAATAAATACTTTAAAGCAGCTGTTCCCTCC
 CCACCCCAAAAAAAGGATGATTGGAAATGAAGAACGAGGATTCAAAAGAAAAAGATGTTCTATTTTCTC
 TATAAAGGAGAAAGTGAGCGCAAGGAGATATTTTGGAAATGAAAGTTTGGGGCTTTTTAGTAAAGTAAGAAGAACT
 GGTGTGGTGGTGTTTTCTTTCTTTTTGAATTTCCCAAGAGGAGAGGAATTAATAATACATCTGCAAAAGAAA
 TTTGAGAGAGAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGGACAGTTGGA
 TTTGTGCTATGTGTGACTAAAATTGACGGATAATTGTCAGTTGGATTTTTCTTCATCAACCTCTTTTTTTAAAT
 TTTTATCTCTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAACACCTGGATTTCATCTGGATGTGTGT
 GTGATCAGTCTGAAAATACAACTGTTTGAATTCGAAGGACCAACACAGATAAAATTATGAATGTTGAACAAAGAT
 GACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTGT
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
 CCAGTTGAGCAAGTGATTGTGTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
 GCTGAACCTCCATGAGAACCRAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCCTTGGAAATCCT
 ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATGGGGCTTTCAATGTCTGGCGAACCTCAACACTCTGGA
 ACTCTTTGACAAATCGTCTTACTACATCCGAAATGGAGCTTTTGTATACCTTGTCTAACTGAAGGAGCTCTGGTT
 GCGAAACAACCCCATTTGAAGATCCCTTCTTATGCTTTTAAACAGAAATTCCTCTTTGCGCGAGCTAGACTTAGG
 GGAATTGAAAAGACTTTCAATACATCTCAGAAGGTGCTTTGAAGGTCGTCCAACTTGAGGTATTGAACTTGTG
 CATGTGCAACTCTCGGGAATCCCTTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
 TTTATCTGCCATCAGGCTGGCTCTTTCCAGGCTTTGATGCACCTTCAAAAACTGTGGATGATACAGTCCAGAT
 TCAAGTGAATTGAACGGAATGCCCTTTGCAACCTTCAGTCACTAGTGGAGATTCAACTCTGGCACAACAAATCTAAC
 ATTAAGTCCCTCAGACTCTCTTCACTCTGTCATCATAGAGCGGATACATTTTACATCAACCACTTTGGAAGCTG
 TAACCTGTACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCTCCGAACACAGCTTGTGTGGCCCGGTG
 TAACTCTCTCCCAATCTAAAGGGAGGTACATTGGAGAGCTCCAGCAAGATTACTTCACTGATGTCTCGGT
 GATTGTGGAGCCCTCGACACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCCTCCACATC
 CCTGACATCTGTATCTTGGATTATCCAAATGGAAACAGTCATGACACATGGGGCTGTACACATGTATGGTGAAT
 TTCCGTGGGAATACTACTGCTTCAAGCCACCTGAAATGTTACTGACGACCACTACTCTCTTCTTACTTTT
 AACCGTCACAGTAGAGACTATGAAACCGTCTCAGGATGAGGCACGGACACAGATAAACAAATGTGGGTCCCACTCC
 AGTGGTGCATGGGAGACCAACCAATGTGACCACTCTCTCACACCAAGAGCACAAGGTGCAGAGGAAACCTT
 CACCATCCAGTGTACTGATATAAACAGTGGATCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGTGCTGGTCAATTTCTACAAGATGAGGAAGCAGCACC
 TCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTTAATGTGGATGATGAGATTACGGGAGACACACC
 CATGGAAGCCACCTGCCCATGCTGCTATCGAGCATGAGCCTAAATCACTATAACTCATACAAATCTCCCTT
 CAACCAACAACAAGTTAAACAATAAATTCATACACAGTTCACTGATGAACCGTTATTGATCCGAATGAA
 CTCTAAGACAAATGTAACAAGACTCAAACTTAAACATTTACAGAGTTCAAAAAACAAACAAATCAAAAAAAA
 GACAGTTTATTAATAATGACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA
 AAAAGAAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAGCAGACAAAA

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FIGURE 104

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVAGLVRAQTCPSCSCSNQFSKVIC
VRKNLREVPDGISTNTRLNLNHNQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIVLSDGTNLNFTNVTVQDGTMYTCMVSNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNTTSLTPQ
STRSTEKTFTIPVTDINSGIGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHQRN
HHAPTRTVEIINVDDIETGDTPMESHLPMPAIEHEHLNHNYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

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FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCTCTGTTTGGGGGCA
TGAAGGGCTTCGGCGCCGGGATTAAGAAGGAATTGACCGGCGAGCGAGGAGGAGCGCGACGCGACGCG
GAGGCGCGGCGTGCACCTCTCGCTTGGAACTTTGTGCGGGCCCGAGACGCGCGCGCTGGAGCTTCGGGTAGA
GACCTAGGCGCGTGCAGCCGCTAGGCGCGCCGAGCCTCCGTGCGCGCGCGGGGTGGGGCTGCTGCTGTGTC
CGCGTGTGGGGCGGCTGCGCGGTCCGACAGCGCGCGTGCGGGGAACTCGGCGAGCCCTCTGGGTAGCCGCG
GAGCGCCCACTCGCCCTACTCTGCGCGCTGCTCGGGGACCTTGCTGGACTCGAGCTCGTAAGCGGCTAGCGCGTCT
CCCGAGCACTCCGCTGCTGGGTGCTCGCTGGAGCTTAAGTCACACAGATTATCTTTACAGCAATCTGAAAGAG
TTGAGGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACATGAATTGGAGACCACTTCAAATCTGGGACCA
GTCTCGGCAAAATATTACACTTCTCTCTGCTGGCTGGAGAACAGGATTGTGAAATACCTCCCTGAAACATCTGAAAGAG
TTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTACAGAGCTCCAACTGCAATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACTCGGGTATTTTGACAAATTTGGGCGAACACA
CTCCTTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAGATGTTTAAACTGCCCCAACTCGAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGAGTGCATTCCAAGGCCCTGGTGTCTCGAAGCT
CTGAAAATGCAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAATTTTG
CAGCTGGACCAATAACCACTTAACAGAGATTACCAAAGGCTGGCTTTACGCTTGTGTAGTCTGCGAGGAACCTCAT
CTCAGCGCAAAATGCCATCAACAGGATCAGCCCTGATGCTCGGGAGTTCTGCGCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTAAAGGTTAGATGATTCAAGCTTCTTGCGCTTAAGCTTACTAAATCACTGCACATTTGGG
AACACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTTCCAGTTTAAAGACTTTTGGATCTGAAGAACA
AATGAAATTTCTCGGACTTTGAAGACATGAATGGTGTCTTCTCGGGCTTGACAACTGAGGCGACTGATATCT
CAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCAATGGAGCATCTAGACCTGAGT
GACAAACGAATAGTGTCTTTCACAGGCAATGCAATTTTCAAAATGAAGAACTGCACAACTTGCATTTTAAATACA
TCAGGCTTTTGTGCGATTTGCCAGCTTAAATGGCTCCCAAGTGGGTGGCGGAAACCACTTTGACAGCTTTTGTGA
AATGCAAGTTGTGCGACTCTCAGCTGCTAAAGGAAGAACATTTTGTCTGTAGCCAGAGTTCGATTTGTGTAT
GATGATTTTCCCAAAACCGAGTACAGGTTTCAAGCAAGAAACAGCTCGGCAATAAAGGTTTCAATTTTGGATTTT
ATCTGCTTACGCTGCGAGCAGCAGTGATTTCCCAATGACTTTTGTCTGGAAAGAAACAAATGAACATCTGCAATGAT
GCTGAAATGGAATTTTGCACACACTCCGGGCGCAAGGTGGCAGGTGATGGAGTATACACCATCTCTCTCGGCT
CGCGAGGTGGAATTTTGCAGTGAAGGGAATAATCCAGTGTGTCATCTCAATCACTTTGGTCTACTCTACTCTGTC
AAAGCCAGCTTACAGTAAATATGCTTCCCTATTCAACAGAGCCCCATGATCTCAACCTCGAGCTGGGGCC
ATGGCAGCTTTGGATGTGCTGTCTGTGGGCGACCGAGCCCCAGATGAGCTGGCAGGAAGTGGGGGACAGAC
TTCCAGCTGCGCGGAGAGACGCATGTCATGTGATGCCGAGGATGACGTGTTCTTATCTGTGATGTGAAGATA
GAGGACATTTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAAGCAATGCAACTCTGACTGTCT
CTAGAAACACCATCATTTTTCGGGCGACTGTTGACCGAACTGTAACCAAGGCGAAACAGCCGCTCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCTCTAACTGAATGAGCAACAGATGATAGCCCATTTGGGTGATACAGAGGCAC
TTTTTTGCGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGAGTGTGAGTGTGGGAAATACAGATGTGAG
ATGTCTAAACACCTTTGACATCAGAGAGGAAACGTGCGCTCAGTGTGATCCCACTCCAACTCGCGACTCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGCGGCTGCGGCTGTGCTGATCATAGCCGCTGCTGTGCTGT
GTGTTGGGCGACGTCACTCGTGTGGGTGTTCATATACACACAAGGCGGAGGAATGAAGATTTGCGACATTTACC
AACACAGATGAGACCACTTGCACGAGATATTCCTAGTATTGTCTATCTCAGGGAACGTTAGCTGACAGGCGAG
GATGGGTACGTGCTCTCAGAAAGTGAAGGCCACCACTGTTGTCACTCTCAGGTGTCTGGAATTTTCTTACCA
CAACTAGCAGTAGAGGGGACCTCCATATTGACAAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCT
CTTTGTCGGTTTTTGGGATCCACAGGCCCTATGTAATTGAAGGAAATGTGATGCGCTCAGATCTTTTGAAGAA
TATCATACAGTTTGCAGTCTGCACCGACAGGACTTTTAAAGGCACTATGAGCCAGTGAACAGGACCTTTTAT
GAGTGTACCACTTCTTCTATCTCAGAGAATCTCTGCAAGCAGGACTTCAGTAAATATATCTGCTGGGCTCCAT
GTGAGGAAGCTACTTTACACTGATCTCTCAACTGAAGGACCTGGAATGAAAACTCTGTGCTTAAACAAAGTTC
TCTTTAGATTTTATGTCAAATCAGAGGACGCGCTCGGTGTCTCGAGTAAATCTTTTATGGGTACCTTTTGAAGAA
GCTCTCAGGAACCTCAGCTAGATGCTTAAAGGCTTAAAGGCTTTTGAAGCAGCTGATGAGCCAGTGAACAGGCTTTTAT
TGAAGGCTCATTTCTTCCCGAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAGAAAGGACAGATTTTCAAGAA
GAAATCACTATTGCTTTTAAAGCAGCTTTAGAAAACTACAGGACTCCAACTTTTCACTTTATGCTTGGAC
ACTAGACTGAATGAGACCAAGGAAAGCTTAACTACTACTCTCAAGTGAACCTTTTAAAGAGAGAGAGAT
CTTATGTTTTTAAATGAGGTTTATGAATTTTAAAGGATAAAATGCTTTTATATACAGATGAAGCAACCAATATAC
AAAAAGTTTATGAAATTTTATACCTGGGAATGTGCTCATATAAGAAATACCTTTTAAACTATTTTAACTTTG
TTTTTGTCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTTTATGATTTTATGATTTGTCGAGA
TTTCTTTTATGGAATATGATTTACTAAAGCACTTTTAAATATACCTGCTTGTATCACTTTTAAATAGAAAGT
ACTTCATTATATTTTGCACATATATTTTAAATAAATGTGTCAATTTGAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHL SRLDDSSFLGLSLNLT LHI GNNRVSYIADCAFRGLSSKLTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQNAFQOMK
KLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDFF
PKPQITVQPETQSAIKGSNLSFICSAASSDSDPMTFAWKDNEILLHDAEMENYAHLRAGGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGH PAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFRLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIVSDVSDAGKYTCESMNTLGTERGNVRLSVIPTCTDPSQMTAPSLDDDGWA
TVGVVIIAVVCCVGTSLVWVVI IYHTRRRNEDCSITNTDETNL PADIPSYLSSQGT LADRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQHDDSGTCHIDNSS EADVEAATDLFLCPFLGSTGPMY
LKGNVYSGDPFETYHTGCSFDPRTVLMDHYEPSYIKKKCYCPSHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEBPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTGFKALRRPHLDAYS
SPGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDQEEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

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FIGURE 107

CAAAACCTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCGAGCCCGCGGAGCGCAGCTGAGAC
 TGGGGGAGCGCGTTTCGCGCTGTGGGGCGCCGCTTCGGCCCGGGGGCGCAGCAGCGGAAGGCGAAGCTGTGGTCTTGC
 CTGCTCCACGAGGGCGCACTGGTGTGAACCGGGAGAGCCCTGGGTGTCCTTCCCTATCCCTCCTTTATATA
 GAACACTTCCACACTGGGAAGGACGCGGCGAGGAGGAGGGCTCATGGTGAAGCAAGGAGCGCGCTGATCTGCAG
 GCGCACAGCACTTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCGAAGCAAGCTGCCTGGT
 TCCATCAGCCCTTGCGCGCCAGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCGGGGTGCTGTC
 TGCTCTGTGCTGCTGCGGCACAGCTGCACCTGGGACCTGTGCTTGCCTGGAGGGCCCGAGGATTTGGCGGAA
 GTGGCGGGCCAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCGGTGCTGGTACTGAGCCCTGAGG
 AGCCCGGCTTGGCCAGCGCGGTGCTGCTGCCCGGAGACTGTGCTGTTTCCAGGAGGGCGTGGTGAAGCTGTG
 GCGGTATTGACTCGCTGAGTTCCCGGGGGACCTGCTGAGCACACCAACACCTTATCTTGCAGAACAAACAGC
 TGGAAAAGATGACCTTCCGAGGAGCTTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAAACACCGCTGA
 CTTCCCGAGGGCTCCAGAGAGGCGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAAGC
 TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGAATTTGCTGCCAACTATCTCACCAAGATCT
 ATGGGCTCACCTTTGGCCAGAGGCAAACTTGAGGTCTGTGTAACCTGCACAAACAAAGCTGGCAGAGCGCGGGC
 TGCCGGAACAATGTTCAACGGCTCCAGCAAGCTCGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACAGTGC
 CCAAGCACCTCGCCCTGCTGTAACAGCTGCACCTCAAGAACAAACAGCTGGAGAGATCCCCCGGGGGCT
 TCAGCGAGCTGAGCAGCTTGCBCGAGCTATACCTGCAGAACACTACCTGACTGAGCAGGGGCTGGACAAACGAGA
 CTTTCTGGAAGCTCTCCAGCTGGAGTACCTGGATCTGTCCAGCAACACCTGTCTCGGGCTCCAGCTGGGCTGC
 CGCGCAGCTGGTGTCTGTGCACTTTGGAGAAGAACGCCATCCGGAGCTGGAGCGGAATGTGTGACTGACCCGCT
 GCAGCTTGGATCTCTGCTGCTGACAGCAACAGCTCGGGGAGCAGGGCATTCCACCACTGGCTTCCAGGGCC
 TCAAGCGGTGCACACGGTGCACCTGTACAAACACGCGCTGGAGCGGTCGCAAGTGGGCTGCTCGCGCGCTGC
 GCACCTCTATGATCTGCAACACAGATCAGAGCATTTGGCCGCGAAGACTTTGCCAACCACTACTTCTGTGGAG
 AGCTCAACCTCAGCTACAACCACTCAGCAGCCCAAGGTGCACCGCCTCCGCAAGCTGGCGCTGCTGTGCTG
 GCTCGTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCTCGAAATGTCCATGTGTCTGAAG
 TCAAGCGCAATGAGCTGCTGCTTGGCAGCAGGGGGCGCTGGCGGGCATGGCTGCTGAGCTGTGACTCA
 CCAGCAACCGCATGCGCAGCGCTGCTGGGCCCGCTGGCTGGTGGAGCTCGCCCTATCTGACGTCTGTGACA
 TCGCCGGGAATCAGCTCAGAGAGATCCCCGAGGGGCTCCCGAGTCACTTGTAGTACTTGTGACAGAACACA
 AGATTAGTGGGCTGCCCGCCCAATGCTTTCGACTCCACGCCCACTCAAGGGGACTTTTCTCAGTPTTAACAAGC
 TGGCTGTGGGCTCCGTGGTGGACAGTGCTTCCGGAGGCTGAAGCACTTCAGGTCTTGGACATTGAAGGCACT
 TAGAGTTTGTGTGACATTTCCAAGGACCGTGGCGCTTGGGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGG
 AGGAAAGAGGAAACAAGATAGTGACAGGTGATGCAGATGTGACCTAGGATGATGGACCGCGGACTCTTTTCTGC
 AGCACACGCTGTGTGCTGTGAGCCCCCACTTCCGCTGTGCACAGACACACCAAGCTGCACATGAGGCA
 TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCTTCCACGCGCTGTCCACGGCCAGACACATGC
 ACACACATCACACCTCAAAACACCGACTCAGCCACACACAACCTACCTCCAAACACCAAGTCTGTGTACAC
 CCCCACTACCGCTGCCACGCCCTCTGAATCATGAGGGGAAGGGTGTGCCCTCGCTTGGCACACACAGGCACCCA
 TTCCCTCGCCCTGCTGACATGTGTATGCTATGCATACACACACACACATGCACATGCAAGTCAATGTGCGAA
 CAGCCCTCCAAGCCTATGCCACAGACAGCTTTCGCCACGACAGAAATCAGCCATAGCAGCTCGCCGTCTGCTCT
 GTCCATCTGTCCGTCCGTTCCCTGGAGAAAGACACAAGGGTATCCATGCTGTGTGGCAGGTGCTGCCACCCCTCT
 GGAACCTCAAAAGCTATGGCTTTTATTCCTTCCCATCTATGGGGAAGGAGCTCTCAGGACTGCTGGCTGGCC
 TGGCCCACTGCTCTCCAGGTGTGGGCAAGTCACTGTGCTAAGAGTCCCTCCCTCAGCCCTGGCAGGACA
 CAGGCACTTTTCAATGGGCAAGCCAGTGGAGGAGGATGGGAGAGCCCTGGGTGCTGCTGGGGCCTTGGGG
 CAGGAGTGAAGCAGAGTGTATGGGCTGGGCTGAGCCAGGGAGGAAGGACCAAGCTGTGACCTTAGGAGACACTTT
 GTTCTTCAGGCTGTGGGGGAGTTCCGGGTGCTTTATTTTATTTCTTTTCAAGGAAAAAATGATAAAAAAT
 CTCGAAGCTGATTTTCTTGTATTAGAAAAATTAATATAAAGCAATTATCCCTTCCCTGCAAAAAA

FIGURE 108

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPREENEFAEEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFFPGDLP
EHTNHLSLQNNQLEKIYPEELSRHLRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAAANYLTKIYGLTFGQKPNLRSVYLHNKLADAGLPDNMFGSSNV
EVLILSSNPLRHVPKHLPPALYKLHLKNNKLEKIPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNARSVDANVLTPIRSLEYLLHSN
QLREQGIHPLAQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF
LEELNLSYNRITSFQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

03902553.071001

FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCTCGCCGCTGTCTCTCGGGAGCGGCAG
CAGTAGCCCGGGCGCGCAGGGGCTTGGGGGTTCTTCGAGACTCTCAGAGGGGCGGCTCCATCGGGCGCCACACCC
CAACTGTTTCTTCGCGCGCCATCTGCTTCGCGCCCGAGGACCGCTGCCCAACATGGATTTTCTCTGGCGTGGT
GCTGGTATCTCTCGCTCTACCTGCGAGGCGGCGCGGAGTTGCAGCGGGAGGTGGCCAGGCAAAATAGTGTCTATCGAT
TGGCCTATGTCTGTTATGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTGGCCAGTCTTGGGGACAGTGTTCAGCC
TGTGTGCCAACCCAGTGCACCAATGTTGAATGTATCGGGCCAAACAGGTGCAAGTGTCTATCCTGGTTATGTCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCGGCCCTGTAAAGCACAGGTGCATGAACACTTA
CGCGACCTACAAGTGTCTGTCTCAACGATATATGCTCATGCCGGATGTTTCTTGTCTCAAGTGCCTGACCTG
CTCCATGGCAAACTGTGAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTCCAGTGGCCATCCCCTGGCT
GACCTGGCTCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCTCTGCCCTAGATT
TAGCCATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCAATAAAGGCTTCGATCTCATGTATTAATTGAGG
CAAATATCAATGTCTGACATAGACGAATGCTCACTTGGTCAGTATCAAGTGCAGCAGCTTGTCTCGATGTTATAA
CGTACGTGGGTCTTACAAGTGCAAAATGTAAAGAAGGATACCGGGTGTGGAAGTGTGCTGTATATCCCAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAATGGTACCATTAAAGGGTGACACAGGAAA
TAATAATTTGATTCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACACCATAATCTCTCTATCATTACCAA
CAGGCCCTACTTCTAAGCCAAACAAAGACCTACACCAAAGCCAAACCAATTCCTACTCCACCACACCCACC
CCTGCCAACAGAGTCTCAGAACCTCTACCACTCAACCCAGAAAGGCCAACCCGGAGTGAACACTATAGC
ACCAGCTGCCAGTACCTCTCAGGAGGGGATTAAGTGTGACAAAGGGTACAGACAGACCTCAGAAACCCAGAG
AGATGTGTTCAAGTGTCTGCTGACAGTGTGAATTTTGAACATGGACTTGTGGATGGATCAGGGAGAAAGACAA
GGACTTGCAGTGGGAAACCAATCAGGGACCCAGCAGGTGGCAATATCTGAGGAGTGTGGCGCCTCAAGCCCGCAGG
TGCGAAAGCTGACGCGTCTGTGCTCACTCTCGGCGGCTCATGCATTCAGGGAGCTGTGCGTGTCTTCAAGGCA
CAAGGTGCGGGGCGTGCACCTCTGGCACACTCCAGGTGTTTGTGAGAAACACGGTGACACCGAGACGCTGTG
GGGAAAGAAATGGTGGCCATGCTGGGCAACACAGATCACCTTCGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAGATCTATGATGGAATTAAGGAACCTGGATTTAGGCTCTGGAGAG
AGAAGACTGAGGGGCAACCATTTGATGTTTCAAGTATATGAAGGGTTGGCAGAGAGGGTGGCAGCAGCTG
TTCTCCATATGCACTAAGATATAGAACAGAGGAACTGGCTTAGACTAGATATAGGGGAGCATTTCTTGGCAGG
GGCCATGTGTAGAATCTCTATAAAAAAAGAGTGTGAAAAATCTCAGTATCTCTCTCTTTCTAAAAAATTAGA
TAAAAAATTTGTCTAATTTAAGATGTTTAAAGATGTTCTTACCAGGAAAGTAAACAAATATAGAAATTTCCAAA
AGATGTTTGTATCTCTAGTAGTATGTCAGTGAATATCTTAGAACATAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCTAATGGAGAGGGATGAAAGGGGAGAGGCCCAACCAATGCTGAGCTCACTGAATA
TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAAAGGAAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTAGTATCTCAGTAATGCTTCTAGTGTGGCGGTGTTTCAATGTTTCTTCAAGTAAAGGTATAAGCC
TTTCAATTTGTCAATGGATGATGTTTTCAGATTTTTCCTTAAAGAGATCCTTCAAGGAACAAGTTCAGAGAG
ATTTTCTCGGGTGCATTTCTCTGCTCTGTTGTTGTAACAAGTTATCTTGGCTGTGAGAAAGAGTGCCTGGCC
ACACCGCGAGACTTTCTCTCACCTCATCAGTATGATTCAGTTTCTCTTATCAATTTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAACAATAGGTACAATAGAAAGGTTCTTGTCTATTAACTCGTAAAGGCGAGGGCTGG
AGGGGAAAAATAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTAAATGTTTCAAT
TCTTTATGTTGATATTAACCTGACAGCTGAAGATGAAAGGGGAAAAATAATGAAATTTTACTTTTGGATGCCAA
TGATACATTGCATTAACCTGATGGAGAGGTTATCCAAAGTACTGTATAAATCTGTTTATTTATTTAAAGTGT
CTAAATAAAAAATGTTAGTGGTTTTCCAAATGGCTAATAAAAAAATTAATTTGTAATAAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCCQF
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKQIIRCQCPSFGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEYQG
DGLTCVYIPKVMIEPSGPIHVFKGNGTILKGDGTGNNNWIPDVGSTWWPPKTPYIPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPPTGLTTIAPAASTPPGGITVDN
RVQTDPOKPRGDFVSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRLMHSGDLCLSPFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNNGHGWRTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGCCCCCTTTAGATTGTGA
AATGTGGGCTCAAGGTCCTTCAACAACCTTTCTTTCTTTGCAACAGGTGCTTGCTCGGGGGCTGA
AGGTGACAGTGCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTGAGGAAATGGAACCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGAGATTATCTCTCCCT
CTGGGCTGTGGAGTATGTGGGGAACATGACCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCTTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTGCTGAAATGGAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTTCTGATAAAGGGCTAAAGTAGGGGAAGTGTCTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAAATCATTTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT
ATATCCATGTGTCTTCTTCCATGGAATAATATCAACCTACAAAGTTATAAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAGCTCAACACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTGCTTTTCCAGATGTTTCGGTGTTCCTCAGG
ATTTCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTGACAGTACAGT
GTATGAAGTTATTGACGACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTTCATGG
GCTAAACAGTACATTCGAGTGAAATCTGAAGAAACATTTAAGGAAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACACGAGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAATAGAGGCATTTATGCAAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTTCTCATAAGTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAA
TGTGGAACTTTACATTTGTTGATTTTCAGCAGACTTGTTTTATTAATTTTATTAGTG
TTAAGTAATGCAATTTATGTTTCAATTTTATTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAGGATGTTGTACAAAAACAAAACATGCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTGTAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTA
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATCTGTTTTTGTCTTTAAAAA

090205.071001

FIGURE 112

MWLKVF^{TT}FLSFATGACSGLKVTVP^{SHT}VHGV^RGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKS^VVPDLEYQH^KFTMMPPNASLLINPLQ^FPD^EGN^IYIVKVNIQNGT^LSASQ
KIQVT^VDDPVT^KPPV^QIHPPSGAVEYVGNMTLTCHVEGG^TRLAYQWLKNGRPVHTS^TYSFS
PQ^NNTLHIA^PVT^KEDIGNYSCLVRNPVSE^MSDIIMPIIYYGPYGLQVNSDKGLKVG^EVFTV
DLGEAILFDCSADSH^PNTYSWIRRTDNT^TYIIKHGPRLE^VASEKVAQKTMDYVCCAYNNIT
GRQ^ETHFT^VIITSVGLEKLAQKGKSL^SPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRF^ETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQH^IPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

03903653.071001
100710.25520620

FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCAGTTCCCCCTGGCAGTCTCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGAGCAGCGGGCGGCGGAGCAACGTTCCGCGTATCACGGACGAGA
ACTGGAGAGAAGCTGCTGGAAGGAGACTGGATGATAGAAATTTATGCCCGTGGTGCCCTGCT
TGTCAAAACTCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGAGAAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTTATCATTTGAAAGATGGTGAAATTTAGGCGGTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGAAGAGATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATAGGACTCTGTATGATATTTGTGGC
AGATTGCTTTGTCTTCAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATATAAAACAGAAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAAGGTTTCAGTCTAGATTGTCAATTAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTGA AAAAATCGTGCCAAAGCAATAAGATTATGTATATTTGT
TTAATAATAACCTATTTTCAAGTCTGAGTTTGA AAAATTTACATTTCCCAAGTATGCAATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTGTATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTTCAAGTGACAATTTCTGGTCTTTTGAAGGTATATTTCCAAAATTTCTTGT
ATTTTGTAGTTATGCAACTAATAAAAACTACCTTACATTAATTAATACAGTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAAGTTTCATGGTATTTCTCTGATTC
CAACAAAGTTTGATTTTCTCTTGTATTTTCTTACTTACTATGGGTACATTTTTTATTTTT
CAAAATGGATGATAATTTCTTGGAAACATTTTATGTTTTAGTAAACAGTATTTTTTTGTT
GTTTCAAACTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAAAT
TTGGCCACTTTTTTCAAGTTTACATCATTTCTGCTGAACTTCACTTGAATTTGTTTTTT
TTTCTTTTTGGATGTGAAGGTGAACATTTCTGATTTTTGTCTGATGTGAAAAGCCTTGGTA
TTTTACATTTTGA AAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTTCTACTCAGGAAAAAG
CATCTTCTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGAATGCTTGTATTTTAAATAATAACATTTTATATTTTAAAGACAA
ACTTCATATTATCCTGTGTTCTTCTGACTGGTAATATTGTGTGGGATTTACAGGTA AAA
GTCAGTAGGATGGAACATTTTGTGTATTTTACTCCTTAAAGAGCTAGATAACATAGTTTT
CACCTTAAAGAAAGGGGAAAAATCATAAATACAAATGAATCACTGACCATACGTAGTAGAG
AATTTCTGTAATGTCCTTCTTTCTAGGCTCTGTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTTGTAACATT
AAAGATTTGGATGTGTAACCTGTGATGCTTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAGCTGAAAAA AAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCFSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
BEAESKEGTNKDFPQNAIRQRS LGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

0902653.071001

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCCTT
 CTGTGTGCCAGAAACCGCAAGCAGTTGCTAAACCCAGTGGGACAGGCGGATTGGGAAGAGCGGG
 AAGGTCCTGGCCACAGAGCAGTGTGACACTTCCCTCTGTGACC**ATG**AAACTCTGGGTGTCTGC
 ATTGCTGATGGCCCTGGTTTGGTGTCTGTGAGCTGTGTGCAGGCCGAATTCCTCACCTCTATTG
 GGCACATGACTGACCTGATTTATGCAGAGAAAAGAGCTGGTGCGAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAAAGCTTTCCAAGATTAAAGAGCTGGGCCAAACAAAATGGAAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGTCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGAGGACCTTGTCTGCTGCAGGACTCAGCTGCA
 GGTTTTATCGCCAACTCTCTGTGCGAGCGGAGTTCTTCCCCCTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCCCTGCTC
 TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAAACAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
 TCTATGAGAGGCGCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACCA
 TCGTCAGGTACTACGATGTCATGCTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTACTGTCCGACGCTA
 CCGGGTTTCCAAAAGCTCTTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAACAGTAAGACTGCAGAATTGTTACAGGTTGCAAAAT
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTTAGCGGACCTTTTGACAGCGG
 CCTCAAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
 TCTGTGTACAACCTCTTGGGAGCGGGGAAGGTGACTACCGAAACAGACATGCTGCCCTGCCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACT**TGA**CATCCTTTTCTGTCTCTCCCTTCTCTGGTC
 CTTAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTCTATCAGGCT
 GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCCTGT
 GTGACTGAAGTCCAGCCCTTCCATTACGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTCAGTGAACCAAAAGTTCTGATACCTTGTTTACATGTTTGTTTTAT
 GGCATTTCATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

0902353.071004

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP
TDEDEIGAALKMLRLQDTYRLDPGTISRGE LPGTKYQAMLSVDDCFGMGRSAYNEG DYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEBEREKTLTNQTEABLATPEGIYERPVDYLPERDVYESLCRGEVGVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVS KSSWLEEDDDPVVARVNRMRQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFD SGLKTEGNRLATFLNYMSDVEAGGATVPFDLGAAIWPKKGTAVFWYNLLRSGE GDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

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FIGURE 117

GCAGTATTGAGTTTACTTCCCTCTTTTGTAGTGAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TTCAATTATACCGTTTGGCTGGGGTTAGTTCGACACCTTACAGTGTGAAGAGCAGGCAGAAAGAGTTGTGA
AGACAGGACAATCTCTTGGGGATGCTGGTCTGGAAGCCAGCGGCTTGTCTGTCTTTGGGCTCATTGACCC
CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCTGGTGCCTCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGGACACCACTGGCAGGGCTTACCACTAGCGACTGAGCTCCCTGTTGGCTCTGTGCGGCGAGCGCTT
CCCTCATCTTAGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTCTCGATCAGGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTCCAGAGCTCGGCTAGACCAAGTG
ATGAAGACTTCAAAACCCGGATTGTCCCTACTACAGGGACCCCAACAGCCCTACAAGAAAGGTGTCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTGCCGTGAGCGGTTGTGTGGCTGTCTGACCTCCGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTACTCTACTTCACTGGGCAGCGGGGG
CCCGGCTCGCAGGGGATGCAAGTGGTGTCTCATGGGATGAGCGGCCCGCTGGCTCATGTCAAGAGACCTGTC
GCCACCTTCAACACACTTTGGGGCCGACTACGACTGGTTCTTCACTCATGAGGATGACACATATGTGCAAGGCC
CCCGCTGGCAGCCCTGTGCGGCACCTCAGCATCAACCAAGACCTGTACTTAGGCCCGGCAGAGGAGTTTCTG
CGCGAGGCGCAGGCGCCGGTACTGTCTATGGGGCTTTGGCTACCTGTGTGTACGAGGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCGAGGAGACATCTCAGTGGCCCTCTGACGAGTGGCTTGGACGCTGCCCTCATTTG
ACTCTCTGGGCTCGGCTGTCTCTCAGCACCCAGGGGCGAGCATGCTCATTTGAACTGGCCAAAATAGGG
ACCTTGAGAAGGAAGGAGCTGGCTTTCTGAGTGCTTCCGCGTGCACCTGTCTCCGAAGTACCTCATGT
ACCGGCTCCACAAACGCTTACGCGCTCTGAGTGTGAAGCGGCTTACAGTGAATAGAACACTGCAAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCGAAGGGAGGCGAGGCTGAGCTGCGGCTTGGGCTCCCTGTCTCTTTCA
CACCACACTCTGCGCTTTGAGTGTGCGGCTGGGACTACTTCAAGAGCAGCACACTTCTCTCTGCAAGTGGG
CTCCCAAGTGCCACTACAGGGGGCTAGCAGGGCGGAGCTGGTGATGCTCAACGCGCTATCGGCGCTTCGACCCAGCAC
ATCGGCGCTATCAGCCCGCTTGGCTTCCAGAAAGCAGCGACTGTCTCAACGCGCTATCGGCGCTTCGACCCAGCAC
GGGCGATGAGTACACCTGGACCTGTCTGTGGAATGTGTGACACAGCGTGGGCAACGCGCGGCGCTGGCTGCGCA
GGGTGAGCTGTGCGGCCACTGAGCCGGGTGGAATCTTACCTATGCTGCTTGTGCTTGTGCTTGTGCTTGTGCT
TGGAGCCACAGAAATCATTTGCTCACCTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT
ACCCATTCTTTGGGGTAGAGGCTGCAGCAGCGGAGTTAGAGCGACGCTACCTGGGACGAGGCTGGGCTGGCTCG
CTGTGCGAGCAGAGGCGCCCTTCCAGGTGCGACTCATGAGCTGGTCTCGAAGAAGCACCTGTGGACACTCTCT
TCTTCTTACCAACGCTGTGGAAGAAGGCTGGGCGCGAGTCTTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
GGCAGGCTTCTTTTCAGTCCATTTCCAGGAGTTCAATCTGCGCTGTCAACACAGATACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTCCTGTGTGCTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTG
ACCGGACGGCTTCTGCGGAGGGCTGTCTTCAACCGCTGACTACCTGCGGCGCCGAGCCCGCTGGCAGGTGAAC
TGGCAGGCGAGGAAGAGGAGGAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCTCCGCTTCTCAGGCTCC
ACCTCTTTCGGGCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCACCGCTCAGTGAAG
AACTCTACCAACGCTGCGGCTCAGCAACTGGAGGGGCTAGGGGGCGTGCCAGCTGGCTATGGCTCTCTTTG
AGCAGGAGCAGGCGAATAGCACTTAGCCCGCTGGGGGCCCTAACCTCATTACCTTTCCTTTGCTGCCTCAGCC
CCAGGAAGGGCAGGCAAGATGGTGGACAGATAGAGAATGTTGTCTGTATTTTTAAATATGAAATGTTATTAA
ACATGTCTCTGCG

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FIGURE 118

MRLSSLLALLRPALPLIILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSTRARLD
QSDEDFKPRIVPYRDPNPKYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVS HGDERP A WLMSETLRHLHTHFGADYD WFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPD EWLGRCLIDSLGVGCVSQHQGQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLT VLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCP LQGASRADVGDALETALEQLNRRYQPRLRFQKQRLNNGYR
RFD PARGMEYTTDLLLECVTQRGHRRALARRVSLRLPLSRVEILPMPYVTEATRVQVLVPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDFFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKHPVDTLFFLT V WTRPGPEVLNRCRMNAISGWQAFPP
VHFQEFNPALSPQRSPPGPPGAGPDFPSPPGADPSRGAPIGGRFDROQSAEGCFYNADYLA
RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSRLRDCSPRLSEELYHR
CRLSNLEGLGGR AQLAMALFEQE QANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAGAAGATATCTTGAAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAAGAAC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAGGAGACTTGGACCAAACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACTACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAAAACATGAACATTGTAAATG
TGTGGAAAGAAGTGTTTTAAAGAATAATAATTTGCAATAAACTATTATAAATATATATAT
GTGATAAATTTCTAAATTATGAACATTAGAAATCTGTGGGGCACATTTTTTGCTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCAAGTTCCAATGGATTGCGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAGTGAAGTTGAAAAAT

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FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHEHHHLQAPNKEDILKISED
LSKSRVYCIILVKPKDVSLLAAVKETWTKHCDKAFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFATIEENLKYFLKKDPSQPFYLGHTIKSGDLEYVMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMWIKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAAGAGAGGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAAACAAAAAACAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTCCCAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTGCGAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTCACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGTCAAGAAATGTTGTCCATTGAACCTGGGAATATTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCTTACAAGA
AACCTAAAAATGAGAGAGTTTTTTATGGACTGTGAGACCAGGTTGTCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATGGA
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAA
AA
AAAAA

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FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNCSAMGAHLVVINSQBEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQVWDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNVDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

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FIGURE 123

GGGACTACAAGCCGCGCGCGCTGCCGCTGGGCCCTCAGCAACCCCTCGACATGCGCGCTGAGSGCGGCCACCGCGAC
TCCGCTCTGCGCTCGGCTGCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCTGATAGGGGCTGTAAATC
TCAAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACTGTCTTGCATCAITTAACGGATTCCG
AGACAAGTGACCCAGGATCGAGTGGAAAGAAATTCAGATGAACAAACACATATGTGTTTTTTGACAAACAAA
TTCCAGGGAGACTTGGCGGCTCGTGCAGAAATATGSGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCCTGCTGAGGTGCTGTGCTCGAAATGACCGCAAGGAAATGTATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCGTGAACCTGCTGTGTAGAGTGCCGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGATGAGGGCCACCCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCCAATCCAGATTTCGCAATTTCTTTCTTAACTTAAACTCTGAAACAGGCACCTTTGGTGTTCATGTCTG
TTCAACAAGGACGACTCTGGGCACTACTACTGCAATGCTTCCAATGACGCAAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACTGCAACTTGGCGGAATTTATGGGGGGTCTTGGTGTCTTGGTGTCTTCTGCTGTCTG
TCACTGTGGGCATCTGCTGTGCATACAGAGCTGGCTACTTCACTCAACAATAAACAGGATGGAGAAAGTTACAAGA
AACCAGGGAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGCGCACTTCAGACACAAGTCATCGTTTTG
TGATCTGAGACCCCGGCTGGCTGAGAGCGCACAGAGCGCAGCTGCACATACCTCTGCTAGAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGCACAGAGCTAGACACTCAITTCAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACTCAAGCCACATGAATAGAAGAAITTTCTCAAGATGGACCCGGTAAATATAACCAA
GGAAGCGAACTGGGTGGCTTCACTGAGTGGGTCTCTAATCTGTTTCTGGCCGATTCCTCCGATGAGTATTGAG
GTGATCTTAAAGAGTTTGTCTCACTGAAAGCGGCTGCTGGGCCCTGTGAAGCCAGCATGTTCAACACTGGTGT
CAGAGGCCACAGCAGCAGCTGTGAGATGGCAGGTGGCTGGAGCAGCACAGCAGCGCATCCCGGGGGGAACCA
GAAAAGGCTCTTACACAGCAGCTTACTTCTATCGGCCACAGACACCCACGAGTTTCTTCTTAAAGCTCTGC
TGATCGGTGTTGCAAGTGCATTTGTGGAGAAGCTTTTGTGATCAGCATTTTGTAAACACAAATCAGGAAG
GTAAATTTGGTGTGGGAAGAGGATCTTGGCTGAGGAAACCTGCTGTGCAACAGGCTGCAGGATTAAAGGAA
ACCTCTGCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGCTCTGTTTATTTATAAATTT
TACATCTAAATTTTGTCAAGGATGATTTTGTATTGATTTGAAAGAAATTTCTATTTAACTGATTAATATTTGT
CATACAATGTTAAATAACCTATTTTAAAAAGAGTTCAACTTAAGGTAGAGTTTCAAGCTACTAGTGTAAAT
TGGAAATATCAATAATTAAGAGTATTTTACCAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTCTTTCT
CACACAAGTTTTAGCCCTTTTTCAAGGGAACCTCATCTGTCTACACATCAGACCACTAGTTGCTTAGGAAACCT
TAAAAATTCAGTTTAAGCAATTTGAAATCAGTTTGATCTCTTCAAAAGAAACCTCTCAGGTAGCTTTGAAC
GCCTCTTCTGAGATGACTAGGACAGCTCTGACCCAGAGGCGCACCCAGAGGCCCTCAGATGTACATACACAGAT
CCAGTCAGCTCCTGGGTTGGCCAGCGCGCCCCGCTCTAGCTCACTGTGCTCCTGCTGTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGTGAGCTTTACTCACTGTCGCTGCTGCTTCACTCAGCAGC
TCTCAGGTGGGCATGCGAGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTGGGGCTCCTGTAAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTAAGTTTGTTTAATTAATTTGTT
AAGATTGTCTAAGGCTCAAAGGCAATTCGGAATCAAGTCTGTCAAGTACAATAACATTTTTAAAAAGAAATGGAT
CCCATGTTCTCTTTGCCACAGAGAAAGCACCCAGAGCGCCACAGGCTCTGTGCAATTTCAAACAAACCATGAT
GGAGTGGCGCAGTCCAGCCCTTTTAAAGAACGCTCAGGTGGAGCAGCCAGGCTGAAAGGCTGGCGGGGAGGAAAG
TGAAAGCGCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCTATCCGCGGAGACACTGCTCCCAT
TGTGGGGGCTATAGCAACTCACTCAGAAGCTGTGCTTCAAGAGCAGGTGTTCTCAGCTCAGATCAATCACTT
CGCGTGTGCTCAGGACTGAGTGAAGCTGTAAAGCAAGGAGCTGTGAGAAGGAGCACTCAACTGTGTGCTTGA
GAATGCTCTCACTCACTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTATACTTTGACAGCTTTTTTTT
AAATGATCATAGAGACTGTGTTGACTTTTTTAGTATTGTAAGACATTTGGCCAGGCGGCTTGGCAGAGGCA
GGAATGCTCTCAGCAGTGGCTGAGTCTTCCCTGGTGTCTGCTGCAATGCACTCTGATGCTCATGATGCAAGTTT
CTCTCATCATGCCACTTGGTAGAGAGGATGGCTCCCAACCTCAGCGTTGGGGATTACGCTCCAGCCTCT
TCTTGTGTGTCTAGTAGAGGTAGCCCTTATTGCCCTCTTCTATACAAACCTCTACAACTGAGGCTGCA
TGGGAACAGGTTGAAAGATGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATTAACCTGAGATAGA
CGGAAGAGATCTCGTGATTTTGAATGTGAATGTGACTCAAGACTCAGGCGCATCAGAGCTGTGATTTG
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACAACCGTAATTTGGCATTGTTTAAAC
CTCATTTATAAAGCTTCAAAAAACCA

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Important features of the protein:

amino acids 1-30

amino acids 243-263

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

amino acids 106-109, 296-299

amino acids 69-77

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267